

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 25, 2004, 14:37:48 ; Search time 55 Seconds
(without alignments)
107.882 Million cell updates/sec

le: US-09-915-914B-7
fect score: 135
uence: 1 KETWETWTEWSQPKKRV 21

ring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

rched: 1586107 seqs, 282547505 residues

al number of hits satisfying chosen parameters: 1586107

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	135	100.0	21	5	ABG78995 Cell pene
2	135	100.0	21	5	ABB77693 Peptide t
3	135	100.0	21	5	ABB77671 Peptide t
4	135	100.0	21	7	ADB68484 Peptide s
5	135	100.0	21	7	ADC22460 Protein-d
6	123	91.1	21	5	ABB77674 Peptide t
7	120	88.9	20	5	ABB77672 Peptide t
8	108	80.0	19	5	ABB77676 Peptide t
9	106	78.5	20	5	ABB77673 Peptide t
10	105.5	78.1	20	5	ABB77694 Peptide t
11	102	75.6	19	5	ABB77675 Peptide t
12	99	73.3	19	5	ABB10106 Peptide t
13	90	66.7	12	5	ABB77689 Hydrophob
14	90	66.7	12	5	ABP56174 Cell-targ
15	90	66.7	21	5	ABB77678 Generic p
16	90	66.7	26	5	ABP56200 Chimeric
17	85	63.0	19	5	ABB77699 Peptide t
18	79	58.5	11	5	ABB77695 Peptide t
19	73	54.1	17	5	ABB77667 Peptide t
20	69	51.1	9	5	ABB77692 Peptide t
21	69	51.1	18	5	ABB77666 Peptide t
22	69	51.1	19	5	ABB77668 Peptide t
23	69	51.1	19	5	ABB77698 Peptide t
24	69	51.1	19	5	ABB77669 Peptide t
25	69	51.1	20	5	ABB77679 Generic p

26	64	47.4	19	5	ABB77670	Abb77670 Peptide t
27	61.5	45.6	430	5	ABP47755	Abp47755 Protein #
28	61.5	45.6	560	4	AAB84201	Aab84201 Amino aci
29	61.5	45.6	560	6	AAG79973	Aag79973 P2C/C38S/
30	61.5	45.6	560	7	ADE29023	Ade29023 HIV-1 RT-
31	61.5	45.6	562	6	ABR44741	Abr44741 Plasmid p
32	61.5	45.6	562	6	ABR44740	Abr44740 Plasmid p
33	61.5	45.6	565	6	ABR44743	Abr44743 Plasmid 7
34	61.5	45.6	724	5	AAU11869	Aau11869 HIV pol p
35	61.5	45.6	739	5	AAU11874	Aau11874 HIV pol p
36	61.5	45.6	760	1	AAP94510	Aap94510 Sequence
37	61.5	45.6	850	4	AAE04792	Aae04792 Human imm
38	61.5	45.6	850	4	AAE04791	Aae04791 Human imm
39	61.5	45.6	850	5	ADE71141	Ade71141 Codon opt
40	61.5	45.6	850	5	ADE71143	Ade71143 Inactivat
41	61.5	45.6	850	6	ABU63365	Abu63365 HIV-1 wil
42	61.5	45.6	850	6	ABU63366	Abu63366 HIV-1 ina
43	61.5	45.6	875	4	AAE04794	Aae04794 Human tPA
44	61.5	45.6	875	4	AAE04793	Aae04793 Human tPA
45	61.5	45.6	875	5	ADE71145	Ade71145 Codon opt

ALIGNMENTS

RESULT 1
ABG78995
ID ABG78995 standard; peptide; 21 AA.
XX
AC ABG78995;
XX
DT 15-NOV-2002 (first entry)
XX
DE Cell penetrating peptide, peptide carrier.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; lymphoma;
KW sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic.
XX
OS Unidentified.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US005212.
XX
PR 15-FEB-2001; 2001US-0268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody.
XX
PS Disclosure; Page 11; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
CC with an antigen, and a pharmaceutically acceptable carrier and (2)
CC preparing a composition for a disease, by providing (I) and CPP
CC associated with an antigen for disease, and introducing the antigen-
CC associated CPP to (I), where antigen enters into the cell. The antigens
CC are, for example, tumour antigen derived epitopes recognised by tumour

infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I or II. The composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ T cells. It is also useful for treating a disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present sequence is cell penetrating peptide of the invention

Sequence 21 AA;

Query Match 100.0%; Score 135; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KETWETWWTWTSQPKKRV 21
|||||
1 KETWETWWTWTSQPKKRV 21

RESULT 2

ABB77693
ABB77693 standard; peptide; 21 AA.

ABB77693;

01-JUL-2002 (first entry)

Peptide transfection agent Pep-2.9-Cya.

Intracellular delivery; transfection agent; cancer; infectious disease; peptide vector.

Synthetic.

WO200210201-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US023406.

31-JUL-2000; 2000US-0221932P.

(ACTI-) ACTIVE MOTIF.
(CNRS) CENT NAT RECH SCI.

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
Horndorp K;

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and hydrophilic domain and having amino acid residues of specified length is useful for a non-covalent association with and transport of a heterologous compound into a cell.

Example 4; Page 77; 156pp; English.

The invention relates to a transfection agent comprises a peptide of about 16 - 30 amino acids in length. Peptides of the invention comprise a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the cellular internalisation of at least one member e.g. peptide, proteins, antibodies, their derivatives

and/or conjugates. They may form part of a pharmaceutical composition to deliver the compound selected from a diagnostic or therapeutic compound, to treat at least one condition such as cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a peptide or inhibitor that disrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the group of the compounds. The agent has a good delivery efficiency for a broad spectrum of compounds and cell types, has a low toxicity, are easy to handle and easy to formulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents the peptide transfection agent Pep-2.9-Cya

Sequence 21 AA;

Query Match 100.0%; Score 135; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETWETWWTWTSQPKKRV 21
|||||
DB 1 KETWETWWTWTSQPKKRV 21

RESULT 3

ABB77671
ABB77671 standard; peptide; 21 AA.

ABB77671;

01-JUL-2002 (first entry)

Peptide transfection agent Pep-2.

Intracellular delivery; transfection agent; cancer; infectious disease; peptide vector.

Synthetic.

WO200210201-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US023406.

31-JUL-2000; 2000US-0221932P.

(ACTI-) ACTIVE MOTIF.
(CNRS) CENT NAT RECH SCI.

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
Horndorp K;

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and hydrophilic domain and having amino acid residues of specified length is useful for a non-covalent association with and transport of a heterologous compound into a cell.

Claim 12; Page 17; 156pp; English.

The invention relates to a transfection agent comprises a peptide of about 16 - 30 amino acids in length. Peptides of the invention comprise a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the cellular internalisation of at least one member e.g. peptide, proteins, antibodies, their derivatives and/or conjugates. They may form part of a pharmaceutical composition to deliver the compound selected from a diagnostic or therapeutic compound,

to treat at least one condition such as cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a peptide or inhibitor that disrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the group of the compounds. The agent has a good delivery efficiency for a broad spectrum of compounds and cell types, has a low toxicity, are easy to handle and easy to formulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents the peptide transfection agent Pep-2

Sequence 21 AA;

Query Match 100.0%; Score 135; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KETWETWTEWSQPKKRV 21
|||||
1 KETWETWTEWSQPKKRV 21

ULT 4
68484

ADB68484 standard; peptide; 21 AA.

ADB68484;

04-DEC-2003 (first entry)

Peptide sequence of Pep-2 peptide transfection agent.

hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
gene expression; respiration; secretion; signalling;
ion-channel activity; cell motility; developmental phenotype;
tumour regression; peptide transfection agent; Pep-2.

Unidentified.

WO2003068798-A2.

21-AUG-2003.

07-FEB-2003; 2003WO-US003904.

09-FEB-2002; 2002US-00072975.

(ACTI-) ACTIVE MOTIF.

Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
WPI; 2003-689653/65.

Method of inhibiting expression of genes or RNA transcripts, useful for therapy and determining effects of genes, by administering oligomers containing hydroxyproline nucleic acid.

Claim 18; Page 184; 240pp; English.

The invention relates to a novel method of inhibiting the expression of one or more genes or RNA transcripts by administering at least one oligonucleotide analogue that includes at least one hydroxyproline nucleic acid (HypNA) monomer to a cell or organism or their extracts. The oligonucleotides of the invention may be used to monitor properties including gene expression, respiration, secretion, signalling, ion-channel activity, cell motility, developmental phenotype and tumour regression. Furthermore, they may be utilised to determine the effects of particular genes, as antisense or homologous recombination constructs e.g. for creating animal models of disease and finally, for increasing the activity of some enzymes, such as polymerases. The current sequence is that of the Pep-2 peptide transfection agent of the invention.

SQ Sequence 21 AA;

Query Match 100.0%; Score 135; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETWETWTEWSQPKKRV 21
|||||
Db 1 KETWETWTEWSQPKKRV 21

RESULT 5

ADC22460

ID ADC22460 standard; peptide; 21 AA.

XX ADC22460;

DT 18-DEC-2003 (first entry)

DE Protein-derived transport peptide SEQ ID NO:309.

XX recombinant fusion protein; fusion protein; binding; detection;
KW localisation domain; binding domain;
KW subcellular compartment localisation.

OS Synthetic.

PN WO2003012068-A2.

PD 13-FEB-2003.

PF 01-AUG-2002; 2002WO-US024572.

PR 01-AUG-2001; 2001US-0309395P.

PR 13-DEC-2001; 2001US-0341589P.

PA (CELL-) CELLOMICS INC.

PI Bright G, Premkumar DR, Chen Y;

DR WPI; 2003-248174/24.

PT New recombinant fusion protein comprising detection and first
localization domains and a binding domain for the molecule of interest,
PT useful for detecting binding of a molecule of interest.

PS Disclosure; SEQ ID NO 309; 101pp; English.

CC The present invention describes a recombinant fusion protein (I) for
detecting binding of a molecule of interest. (I) comprises: (a) a
detection domain; (b) a first localisation domain; and (c) a binding
domain for the molecule of interest. The detection domain, the first
localisation domain and the binding domain for the molecule of interest
constituting the recombinant fusion protein for detecting binding of a
molecule of interest are operably linked. The binding domain for the
molecule of interest is separated from the first localisation domain by 0
-20 amino acid residues. The first localisation domain and the binding
domain for the molecule of interest both do not occur in a single non-
recombinant protein with the same spacing as in the recombinant fusion
protein for detecting binding of a molecule of interest. Also described:
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
CC (2) a recombinant expression vector comprising the nucleic acid control
sequences operably linked to the recombinant nucleic acid molecule; (3) a
genetically engineered host cell transfected with the recombinant
expression vector; (4) a kit for detecting binding of the molecule of
interest; and (5) a method for identifying compounds that alter the
binding of the molecule of interest. The recombinant fusion protein is
useful for detecting binding of a molecule of interest. The recombinant
fusion protein eliminates the need to construct two or more chimeric
proteins and enables the monitoring of biochemical events in live, intact
or fixed cells. The present sequence is used in the exemplification of
CC the present invention.

XX

Sequence 21 AA;
Query Match 100.0%; Score 135; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KETWETWETWETWSQPKKRKV 21
|||||
1 KETWETWETWETWSQPKKRKV 21
SULT 6
B77674
ABB77674 standard; peptide; 21 AA.
ABB77674;
01-JUL-2002 (first entry)
Peptide transfection agent Pep-2.3.
Intracellular delivery; transfection agent; cancer; infectious disease;
peptide vector.
Synthetic.
WO200210201-A2.
07-FEB-2002.
26-JUL-2001; 2001WO-US023406.
31-JUL-2000; 2000US-0221932P.
(ACTI-) ACTIVE MOTIF.
(CNRS) CENT NAT RECH SCI.
Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
Horndorp K;
WPI; 2002-329441/36.
Transfection agent that comprises a peptide comprising hydrophobic and
hydrophilic domain and having amino acid residues of specified length is
useful for a non-covalent association with and transport of a
heterologous compound into a cell.
Claim 12; Page 17; 156pp; English.
The invention relates to a transfection agent comprises a peptide of
about 16 - 30 amino acids in length. Peptides of the invention comprise a
hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
between the domains and a functional group conjugated to at least one
terminal of the peptide. Peptides of the invention are useful for a non-
covalent association with and transport of a heterologous compound into a
cell. They are also useful for promoting the cellular internalisation of
at least one member e.g. peptide, proteins, antibodies, their derivatives
and/or conjugates. They may form part of a pharmaceutical composition to
deliver the compound selected from a diagnostic or therapeutic compound,
to treat at least one condition such as cancer or an infectious disease,
or which targets a cancerous cell or pathogen-infected cell and to
deliver a peptide or inhibitor that disrupts the activity of the enzyme.
The agent of the invention has a transfection efficiency of at least 5%
for at least two of the members of the group of the compounds. The agent
has a good delivery efficiency for a broad spectrum of compounds and cell
types, has a low toxicity, are easy to handle and easy to formulate in
conjunction with the many different compound types that it can deliver.
The peptides are serum sensitive, thus they bode particularly well for
systemic and/or localised in patients. The current sequence represents
the peptide transfection agent Pep-2.3

Sequence 21 AA;

Query Match 91.1%; Score 123; DB 5; Length 21;
Best Local Similarity 90.5%; Pred. No. 7.4e-09;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 KETWETWETWETWSQPKKRKV 21
|||||
Db 1 KETWETWETWETWSQPKKRKV 21
RESULT 7
ABB77672
ID ABB77672 standard; peptide; 20 AA.
XX
AC ABB77672;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.1.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
XX
OS Synthetic.
XX
PN WO200210201-A2.
XX
PD 07-FEB-2002.
XX
PF 26-JUL-2001; 2001WO-US023406.
XX
PR 31-JUL-2000; 2000US-0221932P.
XX
PA (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
XX
XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
PI
XX WPI; 2002-329441/36.
XX
PT Transfection agent that comprises a peptide comprising hydrophobic and
PT hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX
PS Claim 12; Page 17; 156pp; English.
XX
CC The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in
CC conjunction with the many different compound types that it can deliver.
CC The peptides are serum sensitive, thus they bode particularly well for
CC systemic and/or localised in patients. The current sequence represents
XX the peptide transfection agent Pep-2.1
SQ Sequence 20 AA;

Query Match 88.9%; Score 120; DB 5; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.7e-08;

atches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
1 KETWETWTEWSQPKKKR 19
|||||
1 KETWETWTEWSQPKKKR 19

ULT 8
77676
ABB77676 standard; peptide; 19 AA.
ABB77676;

01-JUL-2002 (first entry)

Peptide transfection agent Pep-2.5.

Intracellular delivery; transfection agent; cancer; infectious disease;
peptide vector.

Synthetic.

WO200210201-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US023406.

31-JUL-2000; 2000US-0221932P.

(ACTI-) ACTIVE MOTIF.
(CNRS) CENT NAT RECH SCI.

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
Horndorp K;

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and
hydrophilic domain and having amino acid residues of specified length is
useful for a non-covalent association with and transport of a
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Claim 12; Page 17; 156pp; English.

The invention relates to a transfection agent comprises a peptide of
about 16 - 30 amino acids in length. Peptides of the invention comprise a
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between the domains and a functional group conjugated to at least one
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covalent association with and transport of a heterologous compound into a
cell. They are also useful for promoting the cellular internalisation of
at least one member e.g. peptide, proteins, antibodies, their derivatives
and/or conjugates. They may form part of a pharmaceutical composition to
deliver the compound selected from a diagnostic or therapeutic compound,
to treat at least one condition such as cancer or an infectious disease,
or which targets a cancerous cell or pathogen-infected cell and to
deliver a peptide or inhibitor that disrupts the activity of the enzyme.
The agent of the invention has a transfection efficiency of at least 5%
for at least two of the members of the group of the compounds. The agent
has a good delivery efficiency for a broad spectrum of compounds and cell
types, has a low toxicity, are easy to handle and easy to formulate in
conjunction with the many different compound types that it can deliver.
The peptides are serum sensitive, thus they bode particularly well for
systemic and/or localised in patients. The current sequence represents
the peptide transfection agent Pep-2.5

Sequence 19 AA;

Query Match 80.0%; Score 108; DB 5; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.1e-07;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 WWETWTEWSQPKKKRKV 21
|||||
Db 2 WWETWTEWSQPKKKRKV 19

RESULT 9
ABB77673

ID ABB77673 standard; peptide; 20 AA.

XX ABB77673;

DT 01-JUL-2002 (first entry)

DE Peptide transfection agent Pep-2.2.

KW Intracellular delivery; transfection agent; cancer; infectious disease;
peptide vector.

OS Synthetic.

PN WO200210201-A2.

PD 07-FEB-2002.

PF 26-JUL-2001; 2001WO-US023406.

PR 31-JUL-2000; 2000US-0221932P.

PA (ACTI-) ACTIVE MOTIF.

PA (CNRS) CENT NAT RECH SCI.

PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
Horndorp K;

DR WPI; 2002-329441/36.

PT Transfection agent that comprises a peptide comprising hydrophobic and
hydrophilic domain and having amino acid residues of specified length is
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PS Claim 12; Page 17; 156pp; English.

CC The invention relates to a transfection agent comprises a peptide of
about 16 - 30 amino acids in length. Peptides of the invention comprise a
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terminal of the peptide. Peptides of the invention are useful for a non-
covalent association with and transport of a heterologous compound into a
cell. They are also useful for promoting the cellular internalisation of
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and/or conjugates. They may form part of a pharmaceutical composition to
deliver the compound selected from a diagnostic or therapeutic compound,
to treat at least one condition such as cancer or an infectious disease,
or which targets a cancerous cell or pathogen-infected cell and to
deliver a peptide or inhibitor that disrupts the activity of the enzyme.
The agent of the invention has a transfection efficiency of at least 5%
for at least two of the members of the group of the compounds. The agent
has a good delivery efficiency for a broad spectrum of compounds and cell
types, has a low toxicity, are easy to handle and easy to formulate in
conjunction with the many different compound types that it can deliver.
The peptides are serum sensitive, thus they bode particularly well for
systemic and/or localised in patients. The current sequence represents
the peptide transfection agent Pep-2.2

SQ Sequence 20 AA;

Query Match 78.5%; Score 106; DB 5; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.6e-07;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KETWETWTEWSQPKKKR 19
|||||

1 KETWWTWTEASQPKRK 19

SULT 10
B77694
ABB77694 standard; peptide; 20 AA.

ABB77694;

01-JUL-2002 (first entry)

Peptide transfection agent Pep-2.10-Cya.

Intracellular delivery; transfection agent; cancer; infectious disease;
peptide vector.

Synthetic.
WO200210201-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US023406.

31-JUL-2000; 2000US-0221932P.

(ACTI-) ACTIVE MOTIF.
(CNRS) CENT NAT RECH SCI.

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
Horndorp K;

WPI; 2002-329441/36.

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hydrophilic domain and having amino acid residues of specified length is
useful for a non-covalent association with and transport of a
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Example 4; Page 77; 156pp; English.

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cell. They are also useful for promoting the cellular internalisation of
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and/or conjugates. They may form part of a pharmaceutical composition to
deliver the compound selected from a diagnostic or therapeutic compound,
to treat at least one condition such as cancer or an infectious disease,
or which targets a cancerous cell or pathogen-infected cell and to
deliver a peptide or inhibitor that disrupts the activity of the enzyme.
The agent of the invention has a transfection efficiency of at least 5%
for at least two of the members of the group of the compounds. The agent
has a good delivery efficiency for a broad spectrum of compounds and cell
types, has a low toxicity, are easy to handle and easy to formulate in
conjunction with the many different compound types that it can deliver.
The peptides are serum sensitive, thus they bode particularly well for
systemic and/or localised in patients. The current sequence represents
the peptide transfection agent Pep-2.10-Cya

Sequence 20 AA;

Query Match 78.1%; Score 105.5; DB 5; Length 20;
Best Local Similarity 85.7%; Pred. No. 1.1e-06;
Matches 18; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

1 KETWWTWTEWSQPKRK 21
|||||||
1 KETWWTWTEWSQ-KKRRK 20

RESULT 11
ABB77675
ID ABB77675 standard; peptide; 19 AA.
XX
AC ABB77675;
XX
DT 01-JUL-2002 (first entry)
XX
DE Peptide transfection agent Pep-2.4.
XX
KW Intracellular delivery; transfection agent; cancer; infectious disease;
peptide vector.
XX
OS Synthetic.
XX
PN WO200210201-A2.
XX
PD 07-FEB-2002.
XX
PF 26-JUL-2001; 2001WO-US023406.
XX
PR 31-JUL-2000; 2000US-0221932P.
XX
PA (ACTI-) ACTIVE MOTIF.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX
DR WPI; 2002-329441/36.
XX

Transfection agent that comprises a peptide comprising hydrophobic and
hydrophilic domain and having amino acid residues of specified length is
useful for a non-covalent association with and transport of a
heterologous compound into a cell.

Claim 12; Page 17; 156pp; English.

The invention relates to a transfection agent comprises a peptide of
about 16 - 30 amino acids in length. Peptides of the invention comprise a
hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
between the domains and a functional group conjugated to at least one
terminal of the peptide. Peptides of the invention are useful for a non-
covalent association with and transport of a heterologous compound into a
cell. They are also useful for promoting the cellular internalisation of
at least one member e.g. peptide, proteins, antibodies, their derivatives
and/or conjugates. They may form part of a pharmaceutical composition to
deliver the compound selected from a diagnostic or therapeutic compound,
to treat at least one condition such as cancer or an infectious disease,
or which targets a cancerous cell or pathogen-infected cell and to
deliver a peptide or inhibitor that disrupts the activity of the enzyme.
The agent of the invention has a transfection efficiency of at least 5%
for at least two of the members of the group of the compounds. The agent
has a good delivery efficiency for a broad spectrum of compounds and cell
types, has a low toxicity, are easy to handle and easy to formulate in
conjunction with the many different compound types that it can deliver.
The peptides are serum sensitive, thus they bode particularly well for
systemic and/or localised in patients. The current sequence represents
the peptide transfection agent Pep-2.4

Sequence 19 AA;

Query Match 75.6%; Score 102; DB 5; Length 19;
Best Local Similarity 85.7%; Pred. No. 2.9e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 KETWWTWTEWSQPKRK 21
|||||||
Db 1 KETWWTWTEWSQPKRK 19

RESULT 12

10106
ABB10106 standard; peptide; 19 AA.
ABB10106;

01-JUL-2002 (first entry)

Peptide transfection agent of the invention.

Intracellular delivery; transfection agent; cancer; infectious disease; peptide vector.

Synthetic.

WO200210201-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US023406.

31-JUL-2000; 2000US-0221932P.

(ACTI-) ACTIVE MOTIF.
(CNRS) CENT NAT RECH SCI.

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J; Horndorp K;

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and hydrophilic domain and having amino acid residues of specified length is useful for a non-covalent association with and transport of a heterologous compound into a cell.

Disclosure; Page 154; 156pp; English.

The invention relates to a transfection agent comprises a peptide of about 16 - 30 amino acids in length. Peptides of the invention comprise a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the cellular internalisation of at least one member e.g. peptide, proteins, antibodies, their derivatives and/or conjugates. They may form part of a pharmaceutical composition to deliver the compound selected from a diagnostic or therapeutic compound, to treat at least one condition such as cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a peptide or inhibitor that disrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the group of the compounds. The agent has a good delivery efficiency for a broad spectrum of compounds and cell types, has a low toxicity, are easy to handle and easy to formulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents the peptide transfection agent of the invention. Note: This sequence is present in the sequence listing only, and is not referred to at any point in the specification

Sequence 19 AA;

Query Match 73.3%; Score 99; DB 5; Length 19;
Best Local Similarity 72.2%; Pred. No. 6.9e-06;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

2 ETWWTWTWTSQPKKR 19
:|||||:|||||:
1 KTWWTWTWTSQPKKR 18

ULT 13

ABB77689
ID ABB77689 standard; peptide; 12 AA.
AC ABB77689;

01-JUL-2002 (first entry)

Hydrophobic Trp-rich motif for design of the Pep-2 vector.

Intracellular delivery; transfection agent; cancer; infectious disease; peptide vector.

Synthetic.

WO200210201-A2.

07-FEB-2002.

26-JUL-2001; 2001WO-US023406.

31-JUL-2000; 2000US-0221932P.

(ACTI-) ACTIVE MOTIF.
(CNRS) CENT NAT RECH SCI.

Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J; Horndorp K;

WPI; 2002-329441/36.

Transfection agent that comprises a peptide comprising hydrophobic and hydrophilic domain and having amino acid residues of specified length is useful for a non-covalent association with and transport of a heterologous compound into a cell.

Example 3; Page 71; 156pp; English.

The invention relates to a transfection agent comprises a peptide of about 16 - 30 amino acids in length. Peptides of the invention comprise a hydrophobic domain, a hydrophilic domain, optionally a spacer sequence between the domains and a functional group conjugated to at least one terminal of the peptide. Peptides of the invention are useful for a non-covalent association with and transport of a heterologous compound into a cell. They are also useful for promoting the cellular internalisation of at least one member e.g. peptide, proteins, antibodies, their derivatives and/or conjugates. They may form part of a pharmaceutical composition to deliver the compound selected from a diagnostic or therapeutic compound, to treat at least one condition such as cancer or an infectious disease, or which targets a cancerous cell or pathogen-infected cell and to deliver a peptide or inhibitor that disrupts the activity of the enzyme. The agent of the invention has a transfection efficiency of at least 5% for at least two of the members of the group of the compounds. The agent has a good delivery efficiency for a broad spectrum of compounds and cell types, has a low toxicity, are easy to handle and easy to formulate in conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents a hydrophobic Trp-rich motif for design of the Pep-2 vector (see ABB77671). This motif is required for efficient targeting to the cell membrane and for forming hydrophobic interactions with proteins

Sequence 12 AA;

Query Match 66.7%; Score 90; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KETWWTWTWTEW 12
:|||||:
Db 1 KETWWTWTWTEW 12

RESULT 14

256174
ABP56174 standard; peptide; 12 AA.
ABP56174;
28-MAR-2003 (first entry)
Cell-targeting (TARG) peptide pep-1.
Mitochondrial membrane permeabilisation; mitochondrion; PTPC;
permeability transition pore complex; virucide; neuroprotective;
vasotropic; cytostatic; infection; cell death regulation; apoptosis;
mitochondrial permeability transition pore complex modulator; cancer;
apoptogenic; ischaemia; neurodegenerative disease; fulminant hepatitis.
Synthetic.
WO200261105-A2.
08-AUG-2002.
01-FEB-2002; 2002WO-EP001633.
02-FEB-2001; 2001US-0265594P.
(INSP) INST PASTEUR.
(CNRS) CENT NAT RECH SCI.
Edelman L, Jacotot E, Briand J;
WPI; 2002-619260/66.
New chimeric bifunctional molecules that target specific cells and
regulate the apoptosis function of the permeability transition pore
complex of the mitochondria, useful for treating or preventing e.g.
cancer or ischemia.
Claim 6; Page 11; 76pp; English.
The present invention describes a chimeric bifunctional molecule (I)
comprising at least a first functional molecule covalently linked to a
second functional molecule, which is able to modulate the activity of the
permeability transition pore complex (PTPC) of the mitochondria. (I) has
the function of specifically targeting and entering a tissue cell
population. The second functional molecule has the function of
specifically targeting, and inducing or preventing the death of the cells
by apoptosis by regulating the opening or the closing of the PTPC of the
mitochondria or its fragment. (I) has virucide, neuroprotective,
vasotropic and cytostatic activities, and can be used as a mitochondrial
permeability transition pore complex (PTPC) modulator. (I) is useful for
treating or preventing a pathological infection or disease. (I) is also
useful for regulating cell death regulatory molecules, specifically the
apoptogenic function of the PTPC, for treating e.g. cancer, ischaemia,
neurodegenerative diseases, fulminant hepatitis or viral infections. The
present sequence represents a cell-targeting peptide which is given in
the exemplification of the present invention
Sequence 12 AA;
Query Match 66.7%; Score 90; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KETWETWTEW 12
1 KETWETWTEW 12
;SULT 15
;B77678
; ABB77678 standard; peptide; 21 AA.
; ABB77678;

XX 01-JUL-2002 (first entry)
DT Generic peptide transfection agent#2.
XX
DE Intracellular delivery; transfection agent; cancer; infectious disease;
KW peptide vector.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Misc-difference 2 /label= Xaa
FT /note= "Xaa may be any or no amino acid residue"
FT Misc-difference 3 /label= Xaa
FT /note= "Xaa may be any or no amino acid residue"
FT Misc-difference 10 /label= Xaa
FT /note= "Xaa may be any or no amino acid residue"
FT Misc-difference 11 /label= Xaa
FT /note= "Xaa may be any or no amino acid residue"
FT Misc-difference 12 /label= Xaa
FT /note= "Xaa may be any or no amino acid residue"
FT Misc-difference 18 /label= Xaa
FT /note= "Xaa may be any or no amino acid residue"
FT Misc-difference 21 /label= Xaa
FT /note= "Xaa may be any or no amino acid residue"
XX WO200210201-A2.
PN 07-FEB-2002.
XX 26-JUL-2001; 2001WO-US023406.
XX 31-JUL-2000; 2000US-0221932P.
PR (ACTI-) ACTIVE MOTIF.
XX (CNRS) CENT NAT RECH SCI.
XX Divida G, Morris M, Mery J, Heitz F, Fernandez J, Archdeacon J;
PI Horndorp K;
XX WPI; 2002-329441/36.
DR Transfection agent that comprises a peptide comprising hydrophobic and
XX hydrophilic domain and having amino acid residues of specified length is
PT useful for a non-covalent association with and transport of a
PT heterologous compound into a cell.
XX Claim 14; Page 18; 156pp; English.
XX The invention relates to a transfection agent comprises a peptide of
CC about 16 - 30 amino acids in length. Peptides of the invention comprise a
CC hydrophobic domain, a hydrophilic domain, optionally a spacer sequence
CC between the domains and a functional group conjugated to at least one
CC terminal of the peptide. Peptides of the invention are useful for a non-
CC covalent association with and transport of a heterologous compound into a
CC cell. They are also useful for promoting the cellular internalisation of
CC at least one member e.g. peptide, proteins, antibodies, their derivatives
CC and/or conjugates. They may form part of a pharmaceutical composition to
CC deliver the compound selected from a diagnostic or therapeutic compound,
CC to treat at least one condition such as cancer or an infectious disease,
CC or which targets a cancerous cell or pathogen-infected cell and to
CC deliver a peptide or inhibitor that disrupts the activity of the enzyme.
CC The agent of the invention has a transfection efficiency of at least 5%
CC for at least two of the members of the group of the compounds. The agent
CC has a good delivery efficiency for a broad spectrum of compounds and cell
CC types, has a low toxicity, are easy to handle and easy to formulate in

conjunction with the many different compound types that it can deliver. The peptides are serum sensitive, thus they bode particularly well for systemic and/or localised in patients. The current sequence represents a generic peptide transfection agent

Sequence 21 AA;

Query Match 66.7%; Score 90; DB 5; Length 21;
Best Local Similarity 70.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
1 KETWWTWTEWSQPKKPK 20
1 KXXWWTWXXXXSQPKKPK 20

Search completed: February 25, 2004, 14:46:57
time : 57 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 25, 2004, 14:43:43 ; Search time 21 Seconds
(without alignments)
96.192 Million cell updates/sec

le: US-09-915-914B-7
fect score: 135
uence: 1 KETWETWTEWSQPKKRV 21
ring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 283366 seqs, 96191526 residues

al number of hits satisfying chosen parameters: 283366

imum DB seq length: 0
imum DB seq length: 200000000
t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

abase : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	ID	Description
1	61.5	45.6	559	B47175	reverse transcript
2	61.5	45.6	1003	GNVWL	HIV-1 retropepsin
3	61.5	45.6	1003	B44001	HIV-1 retropepsin
4	61.5	45.6	1003	T09440	pol polyprotein -
5	61.5	45.6	1012	GNVWL	HIV-1 retropepsin
6	61.5	45.6	1015	GNVWH3	HIV-1 retropepsin
7	56.5	41.9	902	T01668	pol polyprotein -
8	56.5	41.9	1002	S54378	pol polyprotein -
9	56.5	41.9	1451	B86286	F9L1.15 protein -
10	56.5	41.9	1469	H96622	probable ABC trans
11	56	41.5	691	TVVPAS	large T antigen -
12	56	41.5	695	TVVPTB	large T antigen -
13	55.5	41.1	1002	GNLJND	HIV-1 retropepsin
14	54.5	40.4	688	TVVPTJ	large T antigen -
15	53.5	39.6	708	TVVPT4	large T antigen -
16	53.5	39.6	894	T27007	hypothetical prote
17	53	39.3	455	T48973	cytochrome P450-11
18	53	39.3	689	F83902	beta-galactosidase
19	52	38.5	413	C91229	hypothetical prote
20	52	38.5	413	B86076	hypothetical prote
21	52	38.5	418	S40824	hypothetical 48K p
22	52	38.5	710	T25734	hypothetical prote
23	50.5	37.4	111	AH2530	hypothetical prote
24	50.5	37.4	559	A47175	reverse transcript
25	50.5	37.4	912	S33980	pol polyprotein -
26	50.5	37.4	1003	GNVWA2	HIV-1 retropepsin
27	50	37.0	368	T15492	hypothetical prote
28	50	37.0	581	T38501	hypothetical prote
29	50	37.0	686	AH0104	beta-galactosidase

conserved hypothet
hypothetical prote
hypothetical prote
ecdysone-inducible
chitinase VCA0027
ecdysone-inducible
poly(3-hydroxyalka
glycogen phosphory
hypothetical prote
protein CTRP - mal
hypothetical prote
probable membrane
hypothetical prote
hypothetical prote
hypothetical prote
interleukin-9 rece

ALIGNMENTS

RESULT 1

B47175
reverse transcriptase, AZT-sensitive variant - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1996
C:Accession: B47175
R;Mohri, H.; Singh, M.K.; Ching, W.T.; Ho, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 25-29, 1993
A:Title: Quantitation of zidovudine-resistant human immunodeficiency virus type 1 in the
A:Reference number: A47175; MUID:93126353; PMID:7678340
A:Accession: B47175
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-559 <MOH>
A>Note: sequence extracted from NCBI backbone (NCBIP:122099)
C:Superfamily: pol polyprotein

Query Match 45.6%; Score 61.5; DB 2; Length 559;
Best Local Similarity 78.6%; Pred. No. 2.8;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14

Db 395 KETWETWTEYQ 407

RESULT 2

GNVWL
HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Contains: endonuclease (EC 3.1.1.-); retropepsin (EC 3.4.23.16); RNA-directed DNA polym
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Jun-2002
C:Accession: A03966
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03966
A:Molecule type: DNA
A:Residues: 1-1003 <WAI>
C:Comment: Specific enzymatic cleavages may yield mature proteins including protease, re
C:Genetics:
A:Gene: pol
C:Superfamily: pol polyprotein
C:Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleot
F:57-155/Product: retropepsin #status predicted <RTP>
F:81/Active site: Asp (shared with dimeric partner) #status experimental

Query Match 45.6%; Score 61.5; DB 1; Length 1003;
Best Local Similarity 78.6%; Pred. No. 4.9;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
||| |||||:
550 KET-WETWTEYWQ 562

SULT 3

4001

V-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (strain YU-2)
Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
Species: human immunodeficiency virus type 1, HIV-1

Note: host Homo sapiens (man)

Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-Jun-2002

Accession: B44001

Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

Virol. 66, 6587-6600, 1992

Title: Complete nucleotide sequence, genome organization, and biological properties of

Reference number: A44001; MUID:93021387; PMID:1404605

Accession: B44001

Molecule type: DNA

Residues: 1-1003 <LIY>

Cross-references: GB:M93258

Comment: This protein is synthesized as a gag-pol polyprotein.

Comment: Specific enzymatic cleavages may yield mature proteins including proteinase,

Genetics:

Gene: pol

Superfamily: pol polyprotein

Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleot

57-155/Product: retropepsin #status predicted <RTP>

81/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 45.6%; Score 61.5; DB 1; Length 1003;

Best Local Similarity 78.6%; Pred. No. 4.9;

Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14

||| |||||:
550 KET-WETWTEYWQ 562

SULT 4

9440

1 polyprotein - human immunodeficiency virus type 1 (strain JRFL) (fragment)

Species: human immunodeficiency virus type 1, HIV-1

Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-Jan-2000

Accession: T09440

Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

mitted to the EMBL Data Library, July 1996

Reference number: Z16673

Accession: T09440

Status: preliminary; translated from GB/EMBL/DBDJ

Molecule type: DNA

Residues: 1-1003 <PAN>

Cross-references: EMBL:U63632; NID:g1465777; PID:g1465779

Genetics:

Gene: pol

Superfamily: pol polyprotein

Query Match 45.6%; Score 61.5; DB 2; Length 1003;

Best Local Similarity 78.6%; Pred. No. 4.9;

Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14

||| |||||:
550 KET-WETWTEYWQ 562

SULT 5

VWVL

V-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate LV)

Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly

Species: human immunodeficiency virus type 1, HIV-1

Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Jun-2002

C;Accession: A03967

R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.

Nature 313, 450-458, 1985

A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi:

A;Reference number: A93355; MUID:85111157; PMID:2982104

A;Accession: A03967

A;Molecule type: DNA

A;Residues: 1-1012 <MUE>

C;Comment: Specific enzymatic cleavages may yield mature proteins including protease, rev

C;Genetics:

A;Gene: pol

C;Superfamily: pol polyprotein

C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleot

F;66-164/Product: retropepsin #status predicted <RTP>

F;90/Active site: Asp (shared with dimeric partner) #status experimental

Query Match 45.6%; Score 61.5; DB 1; Length 1012;

Best Local Similarity 78.6%; Pred. No. 4.9;

Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14

||| |||||:
559 KET-WETWTEYWQ 571

Db 559 KET-WETWTEYWQ 571

RESULT 6

GNVWH3

HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate HTLV-III,

N;Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA polym

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 03-Jun-2002

C;Accession: A03965

R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorai

nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

Nature 313, 277-284, 1985

A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.

A;Reference number: A93353; MUID:85111123; PMID:2578615

A;Accession: A03965

A;Molecule type: DNA

A;Residues: 1-1015 <RAT>

A;Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA441;

C;Comment: Specific enzymatic cleavages may yield mature proteins including protease, rev

C;Genetics:

A;Gene: pol

C;Superfamily: pol polyprotein

C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleot

F;69-167/Product: retropepsin #status predicted <RTP>

F;93/Active site: Asp (shared with dimeric partner) #status experimental

Query Match 45.6%; Score 61.5; DB 1; Length 1015;

Best Local Similarity 78.6%; Pred. No. 4.9;

Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14

||| |||||:
562 KET-WETWTEYWQ 574

Db 562 KET-WETWTEYWQ 574

RESULT 7

T01668

pol polyprotein - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

C;Accession: T01668

R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell 46, 63-74, 1986

A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolat

A;Reference number: Z14389; MUID:86245056; PMID:2424612

A;Accession: T01668

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-902 <ALI>

Cross-references: EMBL:K03456; NID:G60228; PIDN:CAA28012.1; PID:G60230
Superfamily: pol polyprotein

Query Match 41.9%; Score 56.5; DB 2; Length 902;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

1 KETWETWTWTEWSQ 14
|||||
449 KET-WEAWTEYWQ 461

MULT 8
378
polyprotein - human immunodeficiency virus type 1 (fragment)
Species: human immunodeficiency virus type 1, HIV-1
Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
Accession: S54378
Theodore, T.; Buckler-White, A.J.
Submitted to the EMBL Data Library, July 1989
Reference number: S54377
Accession: S54378
Status: preliminary
Molecule type: genomic RNA
Residues: 1-1002 <THE>
Cross-references: EMBL:M22639; NID:G329377; PIDN:AAA45366.1; PID:G329381
Superfamily: pol polyprotein
Keywords: polyprotein

Query Match 41.9%; Score 56.5; DB 2; Length 1002;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

1 KETWETWTWTEWSQ 14
|||||
549 KET-WETWWVEYWQ 561

MULT 9
286
polyprotein - Arabidopsis thaliana
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 30-Sep-2002
Accession: B86286
Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Lin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
Sen, N.F.; Hughes, B.; Huizar, L.
ature 408, 816-820, 2000
Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
zo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
Reference number: A86141; MUID:21016719; PMID:11130712
Accession: B86286
Status: preliminary
Molecule type: DNA
Residues: 1-1451 <STO>
Cross-references: GB:AE005172; NID:G5103820; PIDN:AAD39650.1; GSPDB:GN00141
Genetics:
Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology;
Map position: 1

Query Match 41.9%; Score 56.5; DB 2; Length 1451;
Best Local Similarity 36.4%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 5; Indels 7; Gaps 1;

1 KETW-----WETWTEWSQP 15
: |||
1170 QNTWGQFKSCLWKQWWTYWRSP 1191

RESULT 10
H96622
probable ABC transporter P23H11.19 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96622
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
arsen, N.F.; Hughes, B.; Huizar, L.
ature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96622
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1469 <STO>
A:Cross-references: GB:AE005173; NID:G5080920; PIDN:AAD39329.1; GSPDB:GN00141
C:Genetics:
A:Gene: P23H11.19
A:Map position: 1

Query Match 41.9%; Score 56.5; DB 2; Length 1469;
Best Local Similarity 36.4%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 5; Indels 7; Gaps 1;

QY 1 KETW-----WETWTEWSQP 15
: |||
Db 1188 QNTWGQFKSCLWKQWWTYWRSP 1209

RESULT 11
TVVPAS
large T antigen - polyomavirus BK (strain AS)
C:Species: Polyomavirus hominis 1 (polyomavirus BK)
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jul-1999
C:Accession: A33278
R:Tavis, J.E.; Walker, D.L.; Gardner, S.D.; Frisque, R.J.
J. Virol. 63, 901-911, 1989
A:Title: Nucleotide sequence of the human polyomavirus AS virus, an antigenic variant of
A:Reference number: A33278; MUID:89095020; PMID:2536111
A:Accession: A33278
A:Molecule type: DNA
A:Residues: 1-691 <TAV>
A:Cross-references: GB:M23122; NID:G332774; PIDN:AAA46878.1; PID:G332775
C:Comment: The DNA sequence was obtained from Genbank, release 61.0.
C:Genetics:
A:Introns: 81/3
C:Superfamily: large T antigen; dnaJ amino-terminal homology
C:Keywords: early protein; glycoprotein
F:12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>
F:78,155/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.5%; Score 56; DB 1; Length 691;
Best Local Similarity 26.7%; Pred. No. 16;
Matches 12; Conservative 4; Mismatches 1; Indels 28; Gaps 2;

QY 5 WETWWT----EWSQ-----PKKKRKV 21
|||
Db 90 WESWSSFNEKWEDELFCHEDMFASDEATADSQHSSTPPKKRKV 134

RESULT 12
TVVPTB
large T antigen - polyomavirus BK
C:Species: Polyomavirus hominis 1 (polyomavirus BK)
C:Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 16-Jul-1999
C:Accession: C03632; C36762; A92981; A03608

Seif, I.; Khoury, G.; Dhar, R.
11 18, 963-977, 1979
Title: The genome of human papovavirus BKV.
Reference number: A03632; MUID:80090082; PMID:229976
Accession: C03632
Molecule type: DNA
Residues: 1-695 <SEI>
Cross-references: GB:V01108; GB:J02038; NID:G60844; PIDN:CAA24300.1; PID:G60849
Experimental source: strain Dunlop
Yang, R.C.A.; Wu, R.
ence 206, 456-462, 1979
Title: BK virus DNA: complete nucleotide sequence of a human tumor virus.
Reference number: A36762; MUID:80058557; PMID:228391
Accession: C36762
Molecule type: DNA
Residues: 1-33,35-259, 'N', 261-334, 'K', 336, 'V', 338-445, 'R', 447-695 <YAN>
Cross-references: GB:V01109; GB:J02039; NID:G60851; PIDN:CAA24302.1; PID:G60852
Experimental source: strain MM
Yang, R.C.A.; Young, A.; Wu, R.
Virol. 34, 416-430, 1980
Title: BK virus DNA sequence coding for the t and T antigens and evaluation of methods
Reference number: A92981; MUID:80185151; PMID:6246273
Accession: A92981
Molecule type: DNA
Residues: 1-695 <YA2>
Experimental source: strain MM
Superfamily: large T antigen; dnaJ amino-terminal homology
Keywords: early protein; glycoprotein
12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>
155/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 41.5%; Score 56; DB 1; Length 695;
Best Local Similarity 26.7%; Pred. No. 16;
Matches 12; Conservative 4; Mismatches 1; Indels 28; Gaps 2;
5 WETWWT-----EWSQ-----PKKKRKV 21
|||:::|:|:|
90 WESWSSPNEKWDLEDLFCHEMPASDEEATADSQHSTPPPKKKRKV 134
SULT 13
LJND
V-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate NDK)
Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
Species: human immunodeficiency virus type 1, HIV-1
Note: host Homo sapiens (man)
Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 03-Jun-2002
Accession: JQ0067
Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
ne 81, 275-284, 1989
Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immuno
Reference number: JQ0065; MUID:90034200; PMID:2806917
Accession: JQ0067
Molecule type: DNA
Residues: 1-1002 <SPI>
Cross-references: GB:M27323; NID:G328154; PIDN:AAA44869.1; PID:G328158
Comment: Specific enzymatic cleavages may yield mature proteins including protease, re
Genetics:
Gene: pol
Superfamily: pol polyprotein
Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucle
56-154/Product: retropepsin #status predicted <RTP>
80/Active site: Asp (shared with dimeric partner) #status predicted
Query Match 41.1%; Score 55.5; DB 1; Length 1002;
Best Local Similarity 71.4%; Pred. No. 26;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
1 KETWWETWTEWSQ 14
|||||:|
549 KET-WETWWIEYWQ 561

RESULT 14
TVVPTJ
large T antigen - polyomavirus JC
C;Species: Polyomavirus hominis 2 (polyomavirus JC)
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999
C;Accession: A03609
R;Frisque, R.J.; Bream, G.L.; Cannella, M.T.
J. Virol. 51, 458-459, 1984
A;Title: Human polyomavirus JC virus genome.
A;Reference number: A03633; MUID:84268011; PMID:6086957
A;Accession: A03609
A;Molecule type: DNA
A;Residues: 1-688 <FRI>
A;Cross-references: GB:J02226; GB:J02227; EMBL:V01118; NID:G1083524; PIDN:AAA82102.1; PII
C;Superfamily: large T antigen; dnaJ amino-terminal homology
C;Keywords: early protein
F;12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>
Query Match 40.4%; Score 54.5; DB 1; Length 688;
Best Local Similarity 25.6%; Pred. No. 25;
Matches 11; Conservative 5; Mismatches 4; Indels 23; Gaps 1;
QY 2 ETWWETWTEWSQ-----PKKKRKV 21
|||:::|:|:|
Db 91 ESWWNTFNEKWDLEDLFCHEMPASDDENTGSHSTPPPKKKKV 133
RESULT 15
TVVPT4
large T antigen - rhesus polyomavirus
C;Species: Polyomavirus maccacae 1 (rhesus polyomavirus, SV40)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 12-Dec-1997
C;Accession: B03631; B36763; A03607
R;Reddy, V.B.; Thimmappaya, B.; Dhar, R.; Subramanian, K.N.; Zain, B.S.; Pan, J.; Ghosh,
Science 200, 494-502, 1978
A;Title: The genome of simian virus 40.
A;Reference number: A03631; MUID:78159686; PMID:205947
A;Accession: B03631
A;Molecule type: DNA
A;Residues: 1-708 <RED>
R;Fiers, W.; Contreras, R.; Haegeman, G.; Rogiers, R.; van de Voorde, A.; van Heuverswyn,
Nature 273, 113-120, 1978
A;Title: Complete nucleotide sequence of SV40 DNA.
A;Reference number: A36763; MUID:78156432; PMID:205802
A;Accession: B36763
A;Molecule type: DNA
A;Residues: 1-530, 'Y', 532-548, 'P', 550-551, 'P', 553-708 <FIE>
A;Experimental source: strain 776
C;Comment: The initial 82 residues of the large T and small t antigens from SV40 are code
C;Superfamily: large T antigen; dnaJ amino-terminal homology
C;Keywords: acetylated amino end
F;12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>
F;1/Modified site: acetylated amino end (Met) #status experimental
Query Match 39.6%; Score 53.5; DB 1; Length 708;
Best Local Similarity 26.2%; Pred. No. 33;
Matches 11; Conservative 3; Mismatches 3; Indels 25; Gaps 1;
QY 5 WETWWTEWSQ-----PKKKRKV 21
|||:::|:|:|
Db 91 WEQWNAFNEENLFCSEMPSSDDEATADSQHSTPPPKKKRKV 132
Search completed: February 25, 2004, 14:48:48
Job time : 25 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 25, 2004, 14:41:08 ; Search time 12 Seconds
(without alignments)
91.123 Million cell updates/sec

le: US-09-915-914B-7
fect score: 135
uence: 1 KETWETWTEWSQPKKKRV 21

ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

rched: 141681 seqs, 52070155 residues

al number of hits satisfying chosen parameters: 141681

imum DB seq length: 0

imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	61.5	45.6	1003	1	POL_HV1H2 human immun
2	61.5	45.6	1003	1	POL_HV1Y2 human immun
3	61.5	45.6	1007	1	POL_HV1JR human immun
4	61.5	45.6	1015	1	POL_HV1B1 human immun
5	61.5	45.6	1015	1	POL_HV1B5 human immun
6	61.5	45.6	1015	1	POL_HV1BR human immun
7	61.5	45.6	1015	1	POL_HV1PV human immun
8	60.5	44.8	1006	1	POL_HV1MN human immun
9	56.5	41.9	1002	1	POL_HV1EL human immun
10	56.5	41.9	1002	1	POL_HV1MA human immun
11	56.5	41.9	1002	1	POL_HV1RH human immun
12	56.5	41.9	1002	1	POL_HV1Z2 human immun
13	56.5	41.9	1003	1	POL_HV1N5 human immun
14	56.5	41.9	1003	1	POL_HV1OY human immun
15	56	41.5	691	1	TALA_POVBA human immun
16	56	41.5	695	1	TALA_POVBK human immun
17	55.5	41.1	1002	1	POL_HV1ND human immun
18	54.5	40.4	688	1	TALA_POVJC human immun
19	53.5	39.6	708	1	TALA_SV40 human immun
20	52	38.5	413	1	YIHS_ECOLI human immun
21	50.5	37.4	1002	1	POL_HV1U4 human immun
22	50.5	37.4	1003	1	POL_HV1A2 human immun
23	48.5	35.9	692	1	PHSG_AQUAE human immun
24	48	35.6	41	1	LPW_VIBPA human immun
25	48	35.6	468	1	IL9R_MOUSE human immun
26	48	35.6	586	1	TALA_POVBO human immun
27	48	35.6	1019	1	POL_SIVS4 human immun
28	48	35.6	1022	1	POL_SIVSP human immun
29	48	35.6	1054	1	POL_SIVMK human immun
30	48	35.6	1056	1	POL_SIVM1 human immun
31	48	35.6	2298	1	YCF2_LOTJA human immun
32	47.5	35.2	315	1	SECF_SYNY3 human immun
33	47.5	35.2	355	1	HNK1_LYCES human immun

34	47.5	35.2	398	1	HKL1_ARATH	P46639 arabidopsis
35	47.5	35.2	1027	1	POL_SIVCZ	P17283 chimpanzee
36	47	34.8	373	1	PRXC_CALFU	P04963 caldariomyc
37	47	34.8	633	1	GYP3_YEAST	P48566 saccharomyc
38	46.5	34.4	794	1	YE14_YEAST	P39961 saccharomyc
39	46.5	34.4	1058	1	POL_HV2D2	P15833 human immun
40	46	34.1	78	1	YO09_BPL2	P42544 bacterioph
41	46	34.1	229	1	UNG_CHLCV	Q821f7 chlamydom
42	46	34.1	504	1	MATK_NEPAL	Q95gt2 repenthes a
43	46	34.1	506	1	MATK_CALVU	O47143 calluna vul
44	46	34.1	513	1	MATK_CYRRA	Q8wiv4 cyrilla rac
45	46	34.1	567	1	EIL3_ARATH	O23116 arabidopsis

ALIGNMENTS

RESULT 1
POL_HV1H2 STANDARD; PRT; 1003 AA.
ID AC P04585; O09777; Q9WJC5;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
DE Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus.";
RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
RN [2]
RP REVISIONS.
RA Ogata N., Alter H.J., Miller R.H., Purcell R.H.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Chappey C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 57-155.
RX MEDLINE=99043699; PubMed=9827997;
RA Kervinen J., Lubkowski J., Zdanov A., Bhatt D., Dunn B.M., Hui K.Y.,
RA Powell D.J., Kay J., Wlodawer A., Gustchina A.;
RT "Toward a universal inhibitor of retroviral proteases: comparative
RT analysis of the interactions of LP-130 complexed with proteases from
RT HIV-1, FIV, and EIAV.";
RL Protein Sci. 7:2314-2323(1998).
RN [5]
RP STRUCTURE BY NMR OF 57-155.
RX MEDLINE=97022126; PubMed=8868486;
RA Yamazaki T., Hinck A.P., Wang Y.-X., Nicholson L.K., Torchia D.A.,
RA Wingfield P., Stahl S.J., Kaufman J.D., Chang C.-H., Domaille P.J.,
RA Lam P.Y.S.;
RT "Three-dimensional solution structure of the HIV-1 protease complexed
RT with DMP323, a novel cyclic urea-type inhibitor, determined by
RT nuclear magnetic resonance spectroscopy.";
RL Protein Sci. 5:495-506(1996).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 156-595.
RX MEDLINE=96097398; PubMed=8535785;
RA Ren J., Esnouf R.M., Hopkins A.L., Ross C., Jones E.Y., Stammers D.K.,
RA Stuart D.I.;
RT "The structure of HIV-1 reverse transcriptase complexed with
RT 9-chloro-TIBO: lessons for inhibitor design.";
RL Structure 3:915-926(1995).

[7]
X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 156-595.
MEDLINE=96208551; PubMed=8648598;
Hopkins A.L., Ren J., Esnouf R.M., Willcox B.E., Jones E.Y., Ross C.,
Miyasaka T., Walker R.T., Tanaka H., Stammers D.K., Stuart D.I.,
"Complexes of HIV-1 reverse transcriptase with inhibitors of the HEPT
series reveal conformational changes relevant to the design of potent
non-nucleoside inhibitors.";
J. Med. Chem. 39:1589-1600(1996).

[8]
X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 157-694.
MEDLINE=97268683; PubMed=9108091;
Esnouf R.M., Ren J., Hopkins A.L., Ross C.K., Jones E.Y.,
Stammers D.K., Stuart D.I.;
"Unique features in the structure of the complex between HIV-1
reverse transcriptase and the bis(heteroaryl)piperazine (BHAP)
U-90152 explain resistance mutations for this nonnucleoside
inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 94:3984-3989(1997).

[9]
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 157-694.
MEDLINE=98356189; PubMed=9689112;
Ren J., Esnouf R.M., Hopkins A.L., Jones E.Y., Kirby I., Keeling J.,
Ross C.K., Iarder B.A., Stuart D.I., Stammers D.K.;
"3'-Azido-3'-deoxythymidine drug resistance mutations in HIV-1
reverse transcriptase can induce long range conformational changes.";
Proc. Natl. Acad. Sci. U.S.A. 95:9518-9523(1998).
-!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
-!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPIN FAMILY.

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EMBL; K03455; AAB50259.1; ALT_INIT.

EMBL; AF033819; AAC82598.2; -.

PDB; 1REV; 14-OCT-96.

PDB; 1RT1; 21-APR-97.

PDB; 1RT2; 21-APR-97.

PDB; 1RT3; 16-FEB-99.

PDB; 1RTH; 03-APR-96.

PDB; 1RTI; 03-APR-96.

PDB; 1RTJ; 03-APR-96.

PDB; 1BVE; 17-AUG-96.

PDB; 1BVG; 17-AUG-96.

PDB; 1KLM; 18-MAR-98.

PDB; 1A30; 29-APR-98.

PDB; 1ODY; 16-FEB-99.

PDB; 1BV7; 14-JAN-00.

PDB; 1BV9; 12-JAN-00.

PDB; 1BWA; 12-JAN-00.

PDB; 1BWB; 12-JAN-00.

PDB; 1COT; 19-JUL-00.

PDB; 1COU; 19-JUL-00.

PDB; 1C1B; 21-JUL-00.

PDB; 1C1C; 06-SEP-00.

PDB; 1DMP; 12-NOV-97.

PDB; 1DTQ; 20-MAR-00.

PDB; 1DTT; 02-APR-00.

PDB; 1EP4; 27-SEP-00.

PDB; 1EX4; 26-JUL-00.

DR PDB; 1EXQ; 03-NOV-00.
DR PDB; 1FK9; 28-FEB-01.
DR PDB; 1FKO; 28-FEB-01.
DR PDB; 1FKP; 03-NOV-00.
DR PDB; 1HVR; 06-APR-99.
DR PDB; 1HVR; 15-MAY-95.
DR PDB; 1HWR; 23-MAR-99.
DR PDB; 1HXB; 12-MAR-97.
DR PDB; 1JKH; 03-OCT-01.
DR PDB; 1JLA; 03-OCT-01.
DR PDB; 1JLB; 03-OCT-01.
DR PDB; 1JLC; 03-OCT-01.
DR PDB; 1JLF; 03-OCT-01.
DR PDB; 1JLG; 03-OCT-01.
DR PDB; 1JLQ; 22-AUG-01.
DR PDB; 1LW0; 30-OCT-02.
DR PDB; 1LW2; 30-OCT-02.
DR PDB; 1LWC; 30-OCT-02.
DR PDB; 1LWE; 30-OCT-02.
DR PDB; 1LWF; 30-OCT-02.
DR PDB; 1MER; 15-APR-98.
DR PDB; 1MES; 15-APR-98.
DR PDB; 1MET; 15-APR-98.
DR PDB; 1MEU; 15-APR-98.
DR PDB; 1O1W; 18-FEB-03.
DR PDB; 1ODW; 01-APR-97.
DR PDB; 1QBR; 15-OCT-97.
DR PDB; 1QBS; 15-OCT-97.
DR PDB; 1QBT; 15-OCT-97.
DR PDB; 1QBU; 15-OCT-97.
DR PDB; 1RT4; 29-JUL-99.
DR PDB; 1RT5; 29-JUL-99.
DR PDB; 1RT6; 29-JUL-99.
DR PDB; 1RT7; 29-JUL-99.
DR PDB; 1RTD; 12-JAN-00.
DR PDB; 1VRT; 03-APR-96.
DR PDB; 3PHV; 15-JAN-92.
DR HIV; K03455; POL\$HXB2.
DR MEROPS; A02.001; -.
DR InterPro; IPR001969; Asprotease_AS.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_Zn.
DR InterPro; IPR009007; Pept_A_acid.
DR InterPro; IPR001995; Peptidase_A2.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00552; integrase; 1.
DR Pfam; PF02022; Integrase_Zn; 1.
DR Pfam; PF00075; rnaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS00175; ASP_PROT_RETROV; 1.
KW AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase; 3D-structure.
FT CHAIN 57 155
FT ACT_SITE 81 81
FT STRAND 58 59
FT STRAND 66 71
FT TURN 72 73
FT STRAND 74 80
FT TURN 82 83
FT STRAND 88 89
FT STRAND 99 104
FT STRAND 109 122
FT STRAND 126 133
FT STRAND 140 141
FT HELIX 143 146
FT TURN 147 150
FT STRAND 152 154
FT STRAND 167 167

Query Match 45.6%; Score 61.5; DB 1; Length 1003;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
1 KETWWETWTEWSQ 14
||| |||||:|
550 KET-WETWWTEYWQ 562

ULT 2
_HVLJ2
POL_HVLJ2 STANDARD; PRT; 1003 AA.
P35963;
01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
POL.
Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=36377;
[1]
SEQUENCE FROM N.A.
MEDLINE=93021387; PubMed=1404605;
Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
Shaw G.M.;
"Complete nucleotide sequence, genome organization, and biological
properties of human immunodeficiency virus type 1 in vivo: evidence
for limited defectiveness and complementation.";
J. Virol. 66:6587-6600(1992).
-!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
-!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

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EMBL; M93258; -; NOT_ANNOTATED_CDS.
PIR; B44001; B44001.
PDB; 1K6C; 06-FEB-02.
PDB; 1K6P; 06-FEB-02.
PDB; 1K6T; 06-FEB-02.
PDB; 1K6V; 06-FEB-02.
PDB; 1WJA; 13-MAY-98.
PDB; 1WJC; 13-MAY-98.
MEROPS; A02.001; -.
InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR002156; RNaseH.
InterPro; IPR001584; Rve.
InterPro; IPR000477; RVTse.
Pfam; PF00552; Integrase; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00665; rve; 1.
Pfam; PF00077; rvp; 1.

DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
KW AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase; 3D-structure.
FT CHAIN 57 155 PROTEASE.
FT ACT_SITE 81 81 BY SIMILARITY.
SQ SEQUENCE 1003 AA; 113794 MW; D2F7187FE4EE8F49 CRC64;
Query Match 45.6%; Score 61.5; DB 1; Length 1003;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
1 KETWWETWTEWSQ 14
||| |||||:|
550 KET-WETWWTEYWQ 562

QY
Db

RESULT 3
POL_HVLJR
ID POL_HVLJR STANDARD; PRT; 1007 AA.
AC P20875;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 1 (JRCF isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
CC -!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
CC -!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

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EMBL; M38429; AAB03745.1; -.
DR HSSP; P03366; 1HMV.
DR HIV; M38429; POL\$JRCF.
DR MEROPS; A02.001; -.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_Zn.
DR InterPro; IPR009007; Pept_A_acid.
DR InterPro; IPR001995; Peptidase_A2.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00552; Integrase; 1.
DR Pfam; PF02022; Integrase_Zn; 1.
DR Pfam; PF00075; rnaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.

PDB; 1TCX; 07-DEC-96.
PDB; 1WJE; 16-DEC-98.
PDB; 1WJF; 16-DEC-98.
PDB; 2BPV; 23-FEB-99.
PDB; 2BPW; 23-FEB-99.
PDB; 2BPX; 23-FEB-99.
PDB; 2BPY; 23-FEB-99.
PDB; 2BPZ; 23-FEB-99.
HIV; K02012; POL\$BH5.
MEROPS; A02.001; -.
InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR002156; RNaseH.
InterPro; IPR001584; Rve.
InterPro; IPR000477; RVTse.
Pfam; PF00552; Integrase; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00665; rve; 1.
Pfam; PF00077; rvp; 1.
Pfam; PF00078; rvt; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS50175; ASP_PROT_RETROV; 1.
AIDS; Polyprotein; Hydrolyase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase; 3D-structure.
CHAIN 69 167
ACT_SITE 93 93
SEQUENCE 1015 AA; 115015 MW; F79F0CB4A1A92CEE CRC64;
Query Match 45.6%; Score 61.5; DB 1; Length 1015;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
1 KETWETWTEWSQ 14
||| |||||:
562 KET-WETWTEYQ 574

SULT 6
L_HV1BR STANDARD; PRT; 1015 AA.
POL_HV1BR
P03367;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
POL polyprotein [Contains: Protease (Retropoepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
POL.
Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11686;
[1]
SEQUENCE FROM N.A.
MEDLINE=85099333; PubMed=2981635;
Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
"Nucleotide sequence of the AIDS virus, LAV.";
Cell 40:9-17(1985).
[2]
REVIEWS TO 23-35.
MEDLINE=86245056; PubMed=2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
Cell 46:63-74(1986).
[3]
X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE=92190341; PubMed=1799632;
Spinelli S., Liu Q.Z., Alzari P.M., Harel P.H., Poljak R.J.;
"The three-dimensional structure of the aspartyl protease from the
HIV-1 isolate BRU.";

RL Biochimie 73:1391-1396(1991).
CC -1- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
CC and P1' variable, but often Pro.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -1- PTM: Cleavage sites that yield the mature proteins remain to be
CC determined.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; K02013; -; NOT_ANNOTATED_CDS.
DR PDB; 1HHP; 15-OCT-92.
DR PDB; 1A8G; 15-JUL-98.
DR PDB; 1A94; 16-FEB-99.
DR PDB; 1D4S; 12-OCT-99.
DR PDB; 1D4Y; 13-OCT-99.
DR PDB; 1DAZ; 03-MAY-00.
DR PDB; 1DIF; 08-MAR-96.
DR PDB; 1HOS; 31-OCT-93.
DR PDB; 1HPO; 21-APR-97.
DR PDB; 1HPS; 15-JAN-95.
DR PDB; 1HPX; 08-MAR-96.
DR PDB; 1HSG; 03-APR-96.
DR PDB; 1HTE; 31-JUL-94.
DR PDB; 1HVL; 30-APR-94.
DR PDB; 1UPJ; 14-OCT-96.
DR PDB; 2UPJ; 14-OCT-96.
DR PDB; 7UPJ; 21-APR-97.
DR MEROPS; A02.001; -.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_Zn.
DR InterPro; IPR009007; Pept_A_acid.
DR InterPro; IPR001995; Peptidase_A2.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00552; Integrase; 1.
DR Pfam; PF02022; Integrase_Zn; 1.
DR Pfam; PF00075; rnaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
KW AIDS; Polyprotein; Hydrolyase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase; 3D-structure.
FT CHAIN 69 167
FT ACT_SITE 93 93
FT STRAND 78 82
FT STRAND 87 92
FT TURN 94 95
FT STRAND 100 102
FT STRAND 111 117
FT TURN 118 119
FT STRAND 120 134
FT TURN 135 136
FT STRAND 137 146
FT STRAND 152 153
FT HELIX 155 161
FT TURN 162 162
SQ SEQUENCE 1015 AA; 115031 MW; 164702F074A84394 CRC64;

Query Match 45.6%; Score 61.5; DB 1; Length 1015;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
|||||
562 KET-WETWTEYWQ 574

ULT 7
_HVLVP
POL_HVLVP STANDARD; PRT; 1015 AA.
P03368;
21-JUL-1986 (Rel. 01, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
POL.
Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11700;
[1]
SEQUENCE FROM N.A.
MEDLINE=85111157; PubMed=2982104;
Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
Capon D.J.;
"Nucleic acid structure and expression of the human
AIDS/lymphadenopathy retrovirus.";
Nature 313:450-458(1985).
[2]
REVISION.
Muesing M.A.;
Submitted (XXX-1987) to the HIV data bank.
-!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
-!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

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EMBL; K02083; AAB59867.1; -.
EMBL; X01762; -; NOT_ANNOTATED_CDS.
PIR; A03967; GNVVVL.
PDB; 1A9M; 17-JUN-98.
PDB; 1AJV; 20-AUG-97.
PDB; 1AJX; 17-SEP-97.
PDB; 1G35; 06-JUN-01.
PDB; 1GTM; 08-NOV-96.
PDB; 1HTG; 31-JUL-94.
PDB; 1HVI; 30-APR-94.
PDB; 1KJH; 06-MAR-02.
PDB; 1NPV; 04-FEB-03.
PDB; 1NPW; 04-FEB-03.
HIV; K02083; POL\$PV22.
MEROPS; A02.001; -.
InterPro; IPR001969; Asparticase_AS.
InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001995; Peptidase_A2.

DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00552; Integrase; 1.
DR Pfam; PF02022; Integrase_Zn; 1.
DR Pfam; PF00075; rnaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS00175; ASP_PROT_RETROV; 1.
KW AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase; 3D-structure.
FT CHAIN 69 167 PROTEASE.
FT ACT_SITE 93 93 BY SIMILARITY.
SQ SEQUENCE 1015 AA; 115090 MW; 51529D18EAC2AF89 CRC64;

Query Match 45.6%; Score 61.5; DB 1; Length 1015;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
|||||
Db 562 KET-WETWTEYWQ 574

RESULT 8
POL_HVLMPN STANDARD; PRT; 1006 AA.
ID POL_HVLMPN
AC P05961;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
DE Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RL Virology 164:531-536(1988).
CC -!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
CC and P1' variable, but often Pro.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -!- PTM: Cleavage sites that yield the mature proteins remain to be
CC determined.
CC -!- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
CC KNOWN AS THE RETROPEPSIN FAMILY.

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EMBL; M17449; -; NOT_ANNOTATED_CDS.
DR HSSP; P03366; IRVL.
DR HIV; M17449; POL\$MN.
DR MEROPS; A02.001; -.
DR InterPro; IPR001969; Asparticase_AS.
DR InterPro; IPR001037; Integrase_C.

InterPro; IPR003308; Integrase_Zn.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR002156; RNaseH.
InterPro; IPR001584; Rve.
InterPro; IPR000477; RVTse.
Pfam; PF00552; Integrase; 1.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00077; rvp; 1.
Pfam; PF00078; rvt; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS00175; ASP_PROT_RETROV; 1.
AIDS; Polypeptide; Hydrolyase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase.
CHAIN 60 158 PROTEASE.
ACT_SITE 84 84 BY SIMILARITY.
SITE 565 565 IN-FRAME TERMINATION CODON.
SEQUENCE 1006 AA; 113860 MW; 460C50DF92AF9BB3 CRC64;

Query Match 44.8%; Score 60.5; DB 1; Length 1006;
Best Local Similarity 76.9%; Pred. No. 2.6;
Matches 10; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

1 KETWETWTEWS 13
|||||
553 KET-WETWTEYT 564

SULT 9
_HV1EL
POL HV1EL STANDARD; PRT; 1002 AA.
P04589; Q77906;
13-AUG-1987 (Rel. 05, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
POL polypeptide [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
POL.
Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11689;
[1]
SEQUENCE FROM N.A. PubMed=2424612;
MEDLINE=86245056; Montagnier L., Sonigo P.;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients."
Cell 46:63-74(1986).
-!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
-!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

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EMBL; A07108; CAA00612.1; -
EMBL; K03454; AAA44325.1; ALT_INIT.
HSP; P03366; 1HNV.
HIV; K03454; POL\$ELI.

MEROPS; A02.001; -
InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR002156; RNaseH.
InterPro; IPR001584; Rve.
InterPro; IPR000477; RVTse.
Pfam; PF00552; Integrase; 1.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00077; rvp; 1.
Pfam; PF00078; rvt; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS00175; ASP_PROT_RETROV; 1.
AIDS; Polypeptide; Hydrolyase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase.
CHAIN 56 154 PROTEASE.
ACT_SITE 80 80 BY SIMILARITY.
SEQUENCE 1002 AA; 114002 MW; 5700903B689D3B54 CRC64;

Query Match 41.9%; Score 56.5; DB 1; Length 1002;
Best Local Similarity 71.4%; Pred. No. 8.1;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
|||||
Db 549 KET-WETWAEYQ 561

RESULT 10
POL_HV1MA
ID POL HV1MA STANDARD; PRT; 1002 AA.
AC P04588; Q79582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE POL polypeptide [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11697;
RN [1]
RP SEQUENCE FROM N.A. PubMed=2424612;
RX MEDLINE=86245056; Montagnier L., Sonigo P.;
RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients."
RL Cell 46:63-74(1986).
CC -!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
CC -!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

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EMBL; X04415; CAA28012.1; -
EMBL; A07116; CAA00619.1; -.

PDB; 1HHJ; 31-OCT-93.
HIV; K03456; POL\$MAL.
MEROPS; A02.001; -.
InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR002156; RNaseH.
InterPro; IPR001584; Rve.
InterPro; IPR000477; RVTse.
Pfam; PF00552; Integrase; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00665; rve; 1.
Pfam; PF00077; rvp; 1.
Pfam; PF00078; rvt; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS0175; ASP_PROT_RETROV; 1.
AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase; 3D-structure.
CHAIN 56 154 PROTEASE.
ACT SITE 80 80 BY SIMILARITY.
SEQUENCE 1002 AA; 113537 MW; 569A29D69ACCGAC5 CRC64;

Query Match 41.9%; Score 56.5; DB 1; Length 1002;
Best Local Similarity 71.4%; Pred. No. 8.1;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
|||||
549 KET-WEAWTEYWQ 561

ULT 11
_HVLRH
POL HVLRH STANDARD; PRT; 1002 AA.
P05959;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
POL.
Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
Viruses; Retrovird viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11701;
[1]
SEQUENCE FROM N.A.
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
Wong-Staal F.;
Submitted (XXX-1987) to the HIV data bank.
-!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
-!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

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EMBL; M17451; AAA45053.1; -.

DR HSSP; P04585; 1RTH.
DR HIV; M17451; POL\$SRF.
DR MEROPS; A02.001; -.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_Zn.
DR InterPro; IPR009007; Pept_A_acid.
DR InterPro; IPR001995; Peptidase_A2.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00552; Integrase; 1.
DR Pfam; PF02022; Integrase_Zn; 1.
DR Pfam; PF00075; rnaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS0175; ASP_PROT_RETROV; 1.
KW AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase.
FT CHAIN 56 154 PROTEASE.
FT ACT SITE 80 80 BY SIMILARITY.
SQ SEQUENCE 1002 AA; 113755 MW; 864341718E5C48C2 CRC64;

Query Match 41.9%; Score 56.5; DB 1; Length 1002;
Best Local Similarity 71.4%; Pred. No. 8.1;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
|||||
Db 549 KET-WEAWTEYWQ 561

RESULT 12
POL_HV1Z2
ID POL HV1Z2 STANDARD; PRT; 1002 AA.
AC P12499;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
GN POL.
OS Human immunodeficiency virus type 1 (Z2/CDC-Z34 isolate) (HIV-1).
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11683;
RN [1]
RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.
CC -!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
CC -!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

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DR EMBL; M22639; AAA45366.1; -.
DR PIR; S54378; S54378.
DR PDB; 1E28; 12-SEP-00.

PDB; 1HXW; 04-FEB-98.
PDB; 1PRO; 17-AUG-96.
PDB; 1VIJ; 13-JAN-99.
PDB; 1VIK; 13-JAN-99.
HIV; M22639; POL\$Z2Z6.
MEROPS; A02.001; -.
InterPro; IPR001969; Aspprotease_AS.
InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn.
InterPro; IPR009007; Pept_A_acid.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR002156; RNaseH.
InterPro; IPR001584; Rve.
InterPro; IPR000477; RVTse.
Pfam; PF00552; Integrase; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00665; rve; 1.
Pfam; PF00077; rvp; 1.
Pfam; PF00078; rvt; 1.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS50175; ASP_PROT_RETROV; 1.
AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
Nuclease; Transferase; RNA-directed DNA polymerase; 3D-structure.
CHAIN 56 154
ACT_SITE 80 80
SEQUENCE 1002 AA; 113724 MW; CB4AAC9AB4742315 CRC64;
Query Match 41.9%; Score 56.5; DB 1; Length 1002;
Best Local Similarity 71.4%; Pred. No. 8.1;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
1 KETWETWTEWSQ 14
|||||
549 KET-WETWWEYQ 561
SULT 13
L_HV1N5
POL HV1N5 STANDARD; PRT; 1003 AA.
P12497;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
POL.
Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11698;
[1]
SEQUENCE FROM N.A. (CLONE PNL4-3).
Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
[2]
X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 57-155.
MEDLINE=90354401; PubMed=2201682;
Fitzgerald P.M.D., McKeever B.M., van Middlesworth J.F.,
Springer J.P., Heimbach J.C., Leu C.-T., Herber W.K., Dixon R.A.F.,
Darke P.L.;
"Crystallographic analysis of a complex between human
immunodeficiency virus type 1 protease and acetyl-pepstatin at 2.0-A
resolution.";
J. Biol. Chem. 265:14209-14219(1990).
-!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonoester.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
-!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO

CC CC KNOWN AS THE RETROPEPSIN FAMILY.
CC CC -----
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CC CC use by non-profit institutions as long as its content is in no way
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR EMBL; M19921; AAA44988.1; -.
DR PDB; 5HVP; 15-OCT-91.
DR PDB; 4PHV; 31-OCT-93.
DR PDB; 1B9F; 19-JUL-99.
DR PDB; 1BHL; 28-OCT-98.
DR PDB; 1BI4; 18-NOV-98.
DR PDB; 1BIS; 16-SEP-98.
DR PDB; 1BIU; 16-SEP-98.
DR PDB; 1WJB; 13-MAY-98.
DR PDB; 1WJD; 13-MAY-98.
DR PDB; 2ITG; 12-MAR-97.
DR PDB; 9HVP; 15-JUL-92.
DR HIV; M19921; POL\$NL43.
DR MEROPS; A02.001; -.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_Zn.
DR InterPro; IPR009007; Pept_A_acid.
DR InterPro; IPR001995; Peptidase_A2.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00552; Integrase; 1.
DR Pfam; PF02022; Integrase_Zn; 1.
DR Pfam; PF00075; rnaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
KW AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;
KW Nuclease; Transferase; RNA-directed DNA polymerase; 3D-structure.
FT CHAIN 57 155
FT ACT_SITE 81 81
FT STRAND 58 60
FT STRAND 66 71
FT TURN 72 73
FT STRAND 74 80
FT TURN 82 83
FT STRAND 87 90
FT STRAND 99 105
FT TURN 106 107
FT STRAND 108 122
FT TURN 123 124
FT STRAND 125 134
FT STRAND 140 141
FT HELIX 143 146
FT HELIX 147 149
FT TURN 150 150
FT STRAND 152 154
SQ SEQUENCE 1003 AA; 113535 MW; EB9CDBA30E114A55 CRC64;
Query Match 41.9%; Score 56.5; DB 1; Length 1003;
Best Local Similarity 71.4%; Pred. No. 8.1;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 1 KETWETWTEWSQ 14
|||||
Db 550 KET-WEAWWEYQ 562
RESULT 14
POL_HV1OY

POL HV10Y STANDARD; PRT; 1003 AA.
P20892;

01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
POL polyprotein [Contains: Protease (Retropepsin) (EC 3.4.23.16);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
POL.

Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11699;

[1]

SEQUENCE FROM N.A.

MEDLINE=90148544; PubMed=2559749;

Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
"A highly defective HIV-1 strain isolated from a healthy Gabonese
individual presenting an atypical western blot.";
AIDS 3:707-715(1989).

-!- CATALYTIC ACTIVITY: Specific for a P1 residue that is hydrophobic,
and P1' variable, but often Pro.

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonocester.

-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).

-!- PTM: Cleavage sites that yield the mature proteins remain to be
determined.

-!- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A
HEALTHY GABONESE INDIVIDUAL.

-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.

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EMBL; M26727; AA83392.1; --

HSSP; P03366; 1RVL.

HIV; M26727; POLSOYI.

MEROPS; A02.001; --

InterPro; IPR001969; Aspprotease AS.

InterPro; IPR001037; Integrase_C.

InterPro; IPR003308; Integrase_Zn.

InterPro; IPR009007; Pept_A_acid.

InterPro; IPR001995; Peptidase_A2.

InterPro; IPR002156; RNaseH.

InterPro; IPR001584; Rve.

InterPro; IPR000477; RVTse.

Pfam; PF00552; Integrase; 1.

Pfam; PF02022; Integrase_Zn; 1.

Pfam; PF00075; rnaseH; 1.

Pfam; PF00665; rve; 1.

Pfam; PF00077; rvp; 1.

Pfam; PF00078; rvt; 1.

PROSITE; PS00141; ASP_PROTEASE; 1.

PROSITE; PS00175; ASP_PROT_RETROV; 1.

AIDS; Polyprotein; Hydrolase; Aspartyl protease; Endonuclease;

Nuclease; Transferase; RNA-directed DNA polymerase.

CHAIN 57 155 PROTEASE.

ACT SITE 81 81 BY SIMILARITY.

SEQUENCE 1003 AA; 113718 MW; AFE997A0EDB88A98 CRC64;

Query Match 41.9%; Score 56.5; DB 1; Length 1003;

Best Local Similarity 71.4%; Pred. No. 8.1;

Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

1 KETWTWTWTEWSQ 14

|||||

550 KET-WEAWTEYWQ 562

RESULT 15

TALA_POVEA

ID TALA_POVEA STANDARD; PRT; 691 AA.

AC P14999;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Large T antigen.

OS Polyomavirus BK (strain AS) (BKV).

OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

OX NCBI_TaxID=10631;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89095020; PubMed=2536111;

RA Tavis J.E., Walker D.L., Gardner S.D., Frisque R.J.;

RT "Nucleotide sequence of the human polyomavirus AS virus, an antigenic

variant of BK virus.";

RL J. Virol. 63:901-911(1989).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: Contains 1 J domain.

CC -----

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DR EMBL; M23122; AAA46878.1; --

DR PIR; A33278; TVVPAS.

DR InterPro; IPR001623; DnaJ_N.

DR InterPro; IPR003133; T_Ag_DNA_bind.

DR Pfam; PF00226; DnaJ; 1.

DR Pfam; PF02217; T_Ag_DNA_bind; 1.

DR SMART; SM00271; DnaJ; 1.

DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.

DR PROSITE; PS00076; DnaJ_2; 1.

DR Early protein; Nuclear protein; ATP-binding; DNA-binding;

DNA replication; Zinc-finger.

FT DOMAIN 12 75 J-DOMAIN.

FT ZN_FING 304 322 C2H2-TYPE (ATYPICAL) (BY SIMILARITY).

FT NP_BIND 428 435 ATP (POTENTIAL).

SQ SEQUENCE 691 AA; 80128 MW; 2F26992D3C441A84 CRC64;

Query Match 41.5%; Score 56; DB 1; Length 691;

Best Local Similarity 26.7%; Pred. No. 6.6;

Matches 12; Conservative 4; Mismatches 1; Indels 28; Gaps 2;

OY 5 WETWTWT---EWSQ-----PKKKRKV 21

|||||

Db 90 WESWSSFNKWDLDLFCHEDMFASDBEATADSQHSPPKKRKV 134

Search completed: February 25, 2004, 14:47:21

Job time : 14 secs

GenCore version 5.1.6
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protein - protein search, using sw model

on: February 25, 2004, 14:42:48 ; Search time 39 Seconds
(without alignments)
169.894 Million cell updates/sec

le: US-09-915-914B-7
fect score: 135
nuence: 1 KETWETWTEWSQPKKRV 21

ring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 1017041 seqs, 315518202 residues

al number of hits satisfying chosen parameters: 1017041

imum DB seq length: 0
imum DB seq length: 2000000000
t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- abase :
- 1: sp_archea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	64.5	47.8	433	15 Q79787	Q79787 human immun
2	63	46.7	793	17 Q8TVU1	Q8tvul methanopyru
3	61.5	45.6	212	15 Q9WGU7	Q9wgu7 human immun
4	61.5	45.6	225	15 Q998V3	Q998v3 human immun
5	61.5	45.6	236	15 Q9WGX3	Q9wgx3 human immun
6	61.5	45.6	237	15 Q9WGV0	Q9wgv0 human immun
7	61.5	45.6	237	15 Q9WGV3	Q9wgv3 human immun
8	61.5	45.6	237	15 Q9WGV7	Q9wgv7 human immun
9	61.5	45.6	237	15 Q9WGW5	Q9wgw5 human immun
10	61.5	45.6	237	15 Q9WGW0	Q9wgw0 human immun
11	61.5	45.6	237	15 Q9WGV5	Q9wgv5 human immun
12	61.5	45.6	237	15 Q9WGV9	Q9wgv9 human immun
13	61.5	45.6	237	15 Q9W8H5	Q9w8h5 human immun
14	61.5	45.6	237	15 Q9W9U0	Q9w9u0 human immun
15	61.5	45.6	237	15 Q9WGX6	Q9wgx6 human immun
16	61.5	45.6	237	15 Q9WGW2	Q9wgw2 human immun

Q9wgx5 human immun
Q9wgw1 human immun
Q9wgv2 human immun
Q9wgu8 human immun
Q9wgv6 human immun
Q9wgv6 human immun
Q9wgv8 human immun
Q9wgv3 human immun
Q9wgw4 human immun
Q9wgv1 human immun
Q9wgv4 human immun
Q9dlj8 human immun
Q9idi3 human immun
Q9idi9 human immun
Q9idc7 human immun
Q9idb6 human immun
Q9idb2 human immun
Q9idf2 human immun
Q9idb0 human immun
Q9idj7 human immun
Q9idi8 human immun
Q9idi7 human immun
Q9idd1 human immun
Q9idi6 human immun
Q9idb8 human immun
Q9idi2 human immun
Q9idi4 human immun
Q9idi5 human immun
Q9idd2 human immun

ALIGNMENTS

RESULT 1
Q79787 ID Q79787 PRELIMINARY; PRT; 433 AA.
AC Q79787;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pol polyprotein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Weidt G., Faisst A.C., Sauer mann U., Lueke W., Jentsch K.,
RA Huns mann G.;
RT "Characterization of a new German HIV-1 isolate: HIV-1NH5."
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; L07423; AAA44982.1; -.
DR PIR; A47330; A47330.
DR PIR; B47330; B47330.
DR PIR; C47330; C47330.
DR PIR; D47330; D47330.
DR PIR; F47330; F47330.
DR HSSP; P03366; 1HMV.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00078; rvt; 1.
KW Polyprotein; RNA-directed DNA polymerase; Transferase.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 50231 MW; C8B4405C810EA235 CRC64;

Query Match 47.8%; Score 64.5; DB 15; Length 433;
Best Local Similarity 78.6%; Pred. No. 1.5;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWWTWTEWSQ 14
|||||
409 KET-WETWTEYQG 421

SULT 2
TVU1

Q8TVU1 PRELIMINARY; PRT; 793 AA.

Q8TVU1;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Predicted DNA-dependent DNA polymerase, component of a
thermophile-specific DNA repair system.
MK1297.

Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
Methanopyrus.
NCBI_TaxID=2320;
[1]

SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
EMBL; AE010421; AAM02510.1; -.
InterPro; IPR00160; GGDEF.
PROSITE; PS50887; GGDEF; 1.
Complete proteome.

SEQUENCE 793 AA; 88610 MW; 1954F3E9975A8F63 CRC64;

Query Match 46.7%; Score 63; DB 17; Length 793;
Best Local Similarity 61.5%; Pred. No. 4.1;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

4 WWETWTEWSQPK 16
|||||
711 WWEGWWEELDEPK 723

SULT 3
WGU7

Q9WGU7 PRELIMINARY; PRT; 212 AA.

Q9WGU7;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Polyprotein (Fragment).
POL.

Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
STRAIN=19142-16-polB;
MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
Walker B.D.;
"Frequent detection of escape from cytotoxic T-lymphocyte recognition
in perinatal human immunodeficiency virus (HIV) type 1 transmission:
the ariel project for the prevention of transmission of HIV from
mother to infant.";
J. Virol. 73:3975-3985 (1999).
EMBL; AF121616; AAD28988.1; -.
GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR Pfam; PF00075; rnaseH; 1.
FT NON_TER 1
SQ SEQUENCE 212 AA; 24550 MW; F7756F76D5298EDB CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 212;
Best Local Similarity 78.6%; Pred. No. 1.8;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWWTWTEWSQ 14
|||||
Db 121 KET-WETWTEYWQ 133

RESULT 4

Q998V3 PRELIMINARY; PRT; 225 AA.

Q998V3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pol protein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97DC.KFE45;
RX MEDLINE=20584657; PubMed=11153090;
RA Vidal N., Mulanga-Kabeya C., Nzilambi N., Delaporte E., Peeters M.;
RT "Identification of a complex env subtype E HIV type 1 virus from the
Democratic Republic of Congo, recombinant with A, G, H, J, K, and
RT unknown subtypes.";
RL AIDS Res. Hum. Retroviruses 16:2059-2064 (2000).
DR EMBL; AJ404322; CAC24829.1; -.
DR HSSP; P03366; 1HRH.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR Pfam; PF00075; rnaseH; 1.
FT NON_TER 1
FT NON_TER 225
SQ SEQUENCE 225 AA; 25904 MW; 3EC5744F6FADAF46 CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 225;
Best Local Similarity 78.6%; Pred. No. 1.9;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWWTWTEWSQ 14
|||||
Db 66 KET-WETWTEYWQ 78

RESULT 5

Q9WGX3 PRELIMINARY; PRT; 236 AA.

Q9WGX3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polyprotein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=08106-C6A-5-polB;
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,

Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M., Walker B.D.;
"Frequent detection of escape from cytotoxic T-lymphocyte recognition in perinatal human immunodeficiency virus (HIV) type 1 transmission: the ariel project for the prevention of transmission of HIV from mother to infant."
J. Virol. 73:3975-3985(1999).
EMBL; AF121647; AAD29019.1; -.
HSSP; P03366; 1HRH.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.
InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1.
NON_TER 1 236
NON_TER 236 236
SEQUENCE 236 AA; 26971 MW; 797EFD34F3DB01A9 CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 236;
Best Local Similarity 71.4%; Pred. No. 2;
atches 10; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
|||||:|
120 KET-WETWTDYGQ 132

ULT 6
GV0 Q9WGV0 PRELIMINARY; PRT; 237 AA.
Q9WGV0;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Polyprotein (Fragment).
POL.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
STRAIN=19142-6-polB;
MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J., Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M., Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M., Walker B.D.;
"Frequent detection of escape from cytotoxic T-lymphocyte recognition in perinatal human immunodeficiency virus (HIV) type 1 transmission: the ariel project for the prevention of transmission of HIV from mother to infant."
J. Virol. 73:3975-3985(1999).
EMBL; AF121621; AAD28993.1; -.
HSSP; P03366; 1HRH.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.
InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1.
NON_TER 1 237
NON_TER 237 237
SEQUENCE 237 AA; 27108 MW; BF8991B93E95AEPB CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
atches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
|||||:|
121 KET-WETWTEYWQ 133

ULT 7
GV3 Q9WGV3 PRELIMINARY; PRT; 237 AA.

AC Q9WGV3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polyprotein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=08102-A4-polB;
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J., Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M., Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M., Walker B.D.;
RA "Frequent detection of escape from cytotoxic T-lymphocyte recognition in perinatal human immunodeficiency virus (HIV) type 1 transmission: the ariel project for the prevention of transmission of HIV from mother to infant."
J. Virol. 73:3975-3985(1999).
DR EMBL; AF121624; AAD28996.1; -.
DR HSSP; P03366; 1HRH.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR Pfam; PF00075; rnaseH; 1.
FT NON_TER 1 237
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 27449 MW; A60D9EF956D86C51 CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
|||||:|
Db 121 KET-WETWTEYWQ 133

RESULT 8
Q9WGV3
ID Q9WGV7 PRELIMINARY; PRT; 237 AA.
AC Q9WGV7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polyprotein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=08102-G3-polB;
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J., Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M., Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M., Walker B.D.;
RA "Frequent detection of escape from cytotoxic T-lymphocyte recognition in perinatal human immunodeficiency virus (HIV) type 1 transmission: the ariel project for the prevention of transmission of HIV from mother to infant."
J. Virol. 73:3975-3985(1999).
DR EMBL; AF121628; AAD29000.1; -.
DR HSSP; P03366; 1HRH.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR Pfam; PF00075; rnaseH; 1.
FT NON_TER 1 237

NON_TER 237 237
SEQUENCE 237 AA; 27384 MW; F0E6D1A729FDD3C3 CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
121 KET-WETWTEYWQ 133

SULT 9
WGWS
Q9WGW5 PRELIMINARY; PRT; 237 AA.
Q9WGW5;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Polyprotein (Fragment).
POL.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
STRAIN=02113-B2-6-polB;
MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
Walker B.D.;
"Frequent detection of escape from cytotoxic T-lymphocyte recognition
in perinatal human immunodeficiency virus (HIV) type 1 transmission:
the ariel project for the prevention of transmission of HIV from
mother to infant.";
J. Virol. 73:3975-3985(1999).
EMBL; AF121636; AAD29008.1; -.
HSSP; P03366; 1HRH.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.
InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1.
NON_TER 1
NON_TER 237 237
SEQUENCE 237 AA; 27236 MW; 50FEB2CD2A2739C6 CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
121 KET-WETWTEYWQ 133

SULT 10
WGWO
Q9WGW0 PRELIMINARY; PRT; 237 AA.
Q9WGW0;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Polyprotein (Fragment).
POL.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
STRAIN=08102-M-1-polB;
MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,

RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
RA Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
in perinatal human immunodeficiency virus (HIV) type 1 transmission:
the ariel project for the prevention of transmission of HIV from
mother to infant.";
J. Virol. 73:3975-3985(1999).
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121631; AAD29003.1; -.
DR HSSP; P03366; 1HRH.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR Pfam; PF00075; rnaseH; 1.
DR NON_TER 1
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 27457 MW; 3F521B7E5B1C75AF CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
Db 121 KET-WETWTEYWQ 133

RESULT 11
Q9WGV5
ID Q9WGV5 PRELIMINARY; PRT; 237 AA.
AC Q9WGV5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polyprotein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=02113-B2-3-polB;
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
RA Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
in perinatal human immunodeficiency virus (HIV) type 1 transmission:
the ariel project for the prevention of transmission of HIV from
mother to infant.";
J. Virol. 73:3975-3985(1999).
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121626; AAD28998.1; -.
DR HSSP; P03366; 1HRH.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR Pfam; PF00075; rnaseH; 1.
DR NON_TER 1
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 27262 MW; 4A5BF3C5EE5B2FA7 CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
Db 121 KET-WETWTEYWQ 133

RESULT 12
Q9WGV9

Q9WGV9 PRELIMINARY; PRT; 237 AA.
Q9WGV9; 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCR-2003 (TrEMBLrel. 25, Last annotation update)
Polyprotein (Fragment).

Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI TaxID=11676;

SEQUENCE FROM N.A.
STRAIN=08102-L-3-polB;
MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
Sakamoto D., Kurstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
Walker B.D.;

GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.
InterPro; IPR02156; RNaseH.
Pfam; PF00075; rnaseH; 1.

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Very Match      45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11: Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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1 KETWWETWTSQ 14
121 KET-WETWTEYQ 133

300LT 13
V8H5

Q9W8H5 PRELIMINARY; PRT; 237 AA.
Q9W8H5; (TREMBLrel. 12, Created)
01-NOV-1999
01-NOV-1999 (TREMBLrel. 12, Last sequence update)
01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Polyprotein (Fragment).

Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI TaxID=11676;

121
SEQUENCE FROM N.A.
STRAIN=VARIOUS STRAINS;
MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Walkes B.M., Ruhl D.J.,
Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
Walker B.D.;

GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.

DR InterPro; IPR002156; RNaseH.
DR Pfam; PF00075; rnaaseH; 1.

KW	Polyprotein.	
FT	NON_TER	1
FT	NON_TER	237
SQ	SEQUENCE	237 AA; 27

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Query Match          45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

Qy 1 KETWETWWTENSQ 14
||| ||| ||| ||| : |
Db 121 KET-WETWWTETWYO 133

RESULT 14

Q9W9U0
ID Q9W9U0 PRELIMINARY; PRT; 237 AA.
AC Q9W9U0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Polyprotein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=19142-3-POLB, and 19142-20-POLB;
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,

Query Match 45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred. No. 2;
Matches 11: Conservative 1; Indels 1;
Mismatches 1; Gaps 1;

Qy 1 KETWETWTEWSQ 14
 ||| ||||| : |
 Pb 121 KET-WETWTEYWO 133

RESULT 15

Release ID	Q9WGX6	PRELIMINARY;	PRT; 237 AA.
ID	Q9WGX6		
AC	Q9WGX6;		
DT	01-NOV-1999	(TREMBLrel. 12, Created)	
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Polyprotein (Fragment).		
GN	POL.		
OS	Human immunodeficiency virus 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		

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NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
STRAIN=02113-B7B-2-polB;
MEDLINE=99214336; PubMed=10196293;
Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
Walker B.D.;
"Frequency detection of escape from cytotoxic T-lymphocyte recognition
in perinatal human immunodeficiency virus (HIV) type 1 transmission:
the ariel project for the prevention of transmission of HIV from
mother to infant.";
J. Virol. 73:3975-3985(1999).
EMBL; AF121652; AAD29024.1; -.
HSP; P03366; IHRH.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.
InterPro; IPR002156; RNaseH.
Pfam; PF00075; rnaseH; 1.
NON_TER 1
NON_TER 237 237
SEQUENCE 237 AA; 27335 MW; 8AFCA15760BDAA73 CRC64;

Query Match 45.6%; Score 61.5; DB 15; Length 237;
Best Local Similarity 78.6%; Pred.No. 2;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
121 KETWETWTEYWQ 133
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Search completed: February 25, 2004, 14:48:15
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

on: February 25, 2004, 14:46:03 ; Search time 23 Seconds
(without alignments)
47.137 Million cell updates/sec

le: US-09-915-914B-7
iect score: 135
ience: 1 KETWETWTWETWSQPKKRKV 21

ing table: BLOSUM62
Gapop 10.0 , Gapext 0.5

ched: 389414 seqs, 51625971 residues

al number of hits satisfying chosen parameters: 389414

imum DB seq length: 0
imum DB seq length: 2000000000

:-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

alt No.	Score	Query Match	Length	DB	ID	Description
1	61.5	45.6	427	4	US-09-690-265-1	Sequence 1, Appli
2	61.5	45.6	560	4	US-09-752-652-1	Sequence 1, Appli
3	61.5	45.6	562	3	US-09-117-217-14	Sequence 14, Appl
4	61.5	45.6	562	4	US-09-735-487-14	Sequence 14, Appl
5	61.5	45.6	913	2	US-07-743-357-22	Sequence 22, Appl
6	61.5	45.6	1005	2	US-07-743-357-1	Sequence 1, Appli
7	61.5	45.6	1015	3	US-08-463-210-9	Sequence 9, Appli
8	61.5	45.6	1015	3	US-09-124-900-3	Sequence 3, Appli
9	61.5	45.6	1015	4	US-08-463-028-9	Sequence 9, Appli
10	61.5	45.6	1016	2	US-07-743-357-2	Sequence 2, Appli
11	61.5	45.6	1016	2	US-07-743-357-3	Sequence 3, Appli
12	61.5	45.6	1016	2	US-07-743-357-4	Sequence 4, Appli
13	61.5	45.6	1016	2	US-07-743-357-5	Sequence 5, Appli
14	60.5	44.8	913	2	US-07-743-357-6	Sequence 6, Appli
15	56.5	41.9	1003	2	US-07-743-357-8	Sequence 8, Appli
16	56.5	41.9	1003	2	US-07-743-357-9	Sequence 9, Appli
17	56.5	41.9	1003	2	US-07-743-357-10	Sequence 10, Appl
18	56.5	41.9	1003	4	US-09-309-572-17	Sequence 17, Appl
19	56.5	41.9	1003	4	US-09-718-096-17	Sequence 17, Appl
20	56	41.5	16	4	US-09-296-089-35	Sequence 35, Appl
21	56	41.5	16	4	US-09-057-363C-49	Sequence 49, Appl
22	56	41.5	16	4	US-09-551-976-35	Sequence 35, Appl
23	56	41.5	16	4	US-09-265-107-49	Sequence 49, Appl
24	56	41.5	700	4	US-09-489-039A-13463	Sequence 13463, A
25	54	40.0	389	4	US-09-489-039A-12200	Sequence 12200, A
26	53.5	39.6	136	3	US-09-014-438-2	Sequence 2, Appli
27	53.5	39.6	1310	4	US-09-170-496D-290	Sequence 290, App

28	53.5	39.6	1310	4	US-09-364-425B-55	Sequence 55, Appl
29	53	39.3	16	3	US-08-849-486-9	Sequence 9, Appli
30	52	38.5	418	4	US-09-958-548-1	Sequence 1, Appli
31	50.5	37.4	1004	2	US-07-743-357-7	Sequence 7, Appli
32	49.5	36.7	697	4	US-09-252-991A-27283	Sequence 27283, A
33	49	36.3	347	4	US-09-252-991A-25478	Sequence 25478, A
34	49	36.3	618	4	US-09-134-000C-6538	Sequence 6538, Ap
35	49	36.3	1586	4	US-09-543-681A-5329	Sequence 5329, Ap
36	48.5	35.9	339	4	US-09-148-545-246	Sequence 246, App
37	48.5	35.9	455	4	US-09-252-991A-24979	Sequence 24979, A
38	48.5	35.9	561	2	US-08-756-317-14	Sequence 14, Appl
39	48	35.6	102	4	US-09-702-705-1818	Sequence 1818, Ap
40	48	35.6	102	4	US-09-736-457-1818	Sequence 1818, Ap
41	48	35.6	102	4	US-09-671-325-1818	Sequence 1818, Ap
42	48	35.6	256	4	US-09-355-166-2	Sequence 2, Appli
43	48	35.6	379	1	US-08-164-614A-8	Sequence 8, Appli
44	48	35.6	379	2	US-08-456-489B-8	Sequence 8, Appli
45	48	35.6	401	4	US-09-252-991A-17779	Sequence 17779, A

ALIGNMENTS

RESULT 1
US-09-690-265-1
; Sequence 1, Application US/09690265
; Patent No. 6300351
; GENERAL INFORMATION:
; APPLICANT: Uckun, Fatih A.
; APPLICANT: Mao, Chen
; TITLE OF INVENTION: BETA-FLUOROETHYL THIOUREA COMPOUNDS AND USE
; FILE REFERENCE: 12152.8USC4
; CURRENT APPLICATION NUMBER: US/09/690,265
; CURRENT FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 09/205,167
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-690-265-1

Query Match 45.6%; Score 61.5; DB 4; Length 427;
Best local Similarity 78.6%; Pred. No. 1.3;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTWETWSQ 14
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Db 395 KET-WETWTEYQW 407

RESULT 2
US-09-752-652-1
; Sequence 1, Application US/09752652
; Patent No. 6503123
; GENERAL INFORMATION:
; APPLICANT: Roberts, Grace B.
; APPLICANT: Furfine, Eric S.
; APPLICANT: Porter, David, J.T.
; TITLE OF INVENTION: CONTINUOUS TIME RESOLVED RESONANCE
; TITLE OF INVENTION: ENERGY TRANSFER ASSAY FOR POLYNUCLEIC ACID POLYMERASE
; FILE REFERENCE: PU3761
; CURRENT APPLICATION NUMBER: US/09/752,652
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/167,940
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 560

TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
NAME/KEY: VARIANT
LOCATION: 100
OTHER INFORMATION: Xaa=Leu or Ile
FEATURE:
NAME/KEY: VARIANT
LOCATION: 103
OTHER INFORMATION: Xaa=Lys or Asn
FEATURE:
NAME/KEY: VARIANT
LOCATION: 106
OTHER INFORMATION: Xaa=Val, Ile or Ala
FEATURE:
NAME/KEY: VARIANT
LOCATION: 108
OTHER INFORMATION: Xaa=Val or Ile
FEATURE:
NAME/KEY: VARIANT
LOCATION: 138
OTHER INFORMATION: Xaa=Glu or Lys
FEATURE:
NAME/KEY: VARIANT
LOCATION: 181
OTHER INFORMATION: Xaa=Tyr or Cys
FEATURE:
NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa at position 188 can be Tyr or Cys
FEATURE:
NAME/KEY: VARIANT
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa at position 236 can be Pro or Leu
-09-752-652-1

Query Match 45.6%; Score 61.5; DB 4; Length 560;
Best Local Similarity 78.6%; Pred. No. 1.7;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
1 KETWETWTEWSQ 14
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395 KET-WETWTEYWQ 407

SULT 3
-09-117-217-14
Sequence 14, Application US/09117217
Patent No. 6221578
GENERAL INFORMATION:
APPLICANT: de BETHUNE, Marie-Pierre
APPLICANT: HERTOOGS, Kurt
APPLICANT: PAUWELS, Rudi
TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
TITLE OF INVENTION: HIV POSITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/117,217
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 562
TYPE: PRT
ORGANISM: HIV-HXB2
-09-117-217-14

Query Match 45.6%; Score 61.5; DB 3; Length 562;
Best Local Similarity 78.6%; Pred. No. 1.7;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
1 KETWETWTEWSQ 14
||| |||||:
395 KET-WETWTEYWQ 407

Db 395 KET-WETWTEYWQ 407
RESULT 4
US-09-735-487-14
; Sequence 14, Application US/09735487
; Patent No. 6528251
; GENERAL INFORMATION:
; APPLICANT: de BETHUNE, Marie-Pierre
; APPLICANT: HERTOOGS, Kurt
; APPLICANT: PAUWELS, Rudi
; TITLE OF INVENTION: METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE
; TITLE OF INVENTION: HIV POSITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
; TITLE OF INVENTION: OF HUMAN HIV STRAINS
; FILE REFERENCE: 1377-125P
; CURRENT APPLICATION NUMBER: US/09/735,487
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 09/117,217
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 562
; TYPE: PRT
; ORGANISM: HIV-HXB2
US-09-735-487-14
Query Match 45.6%; Score 61.5; DB 4; Length 562;
Best Local Similarity 78.6%; Pred. No. 1.7;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 KETWETWTEWSQ 14
||| |||||:
Db 395 KET-WETWTEYWQ 407

RESULT 5
US-07-743-357-22
; Sequence 22, Application US/07743357
; Patent No. 5858646
; GENERAL INFORMATION:
; APPLICANT: Kang, Yong C.
; TITLE OF INVENTION: polypeptide having immunological
; TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KIRBY EADES GALE BAKER
; STREET: Box 3432, Station D
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1M 1H8
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/743,357
; FILING DATE: 21-AUG-1991
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA90/00062
; FILING DATE: 23-FEB-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gale, Edwin J.
; REGISTRATION NUMBER: 28,584
; REFERENCE/DOCKET NUMBER: 30924-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 237-6900
; TELEFAX: (613) 237-0045
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:

LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
STRAIN: HXB2
07-743-357-22
Query Match 45.6%; Score 61.5; DB 2; Length 913;
Best Local Similarity 78.6%; Pred. No. 2.8;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
1 KETWETWTEWSQ 14
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459 KET-WETWTEYWQ 471
ULT 6
07-743-357-1
Sequence 1, Application US/077433357
Patent No. 5858646
GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-0045
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1005 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
STRAIN: HXB2
07-743-357-1
Query Match 45.6%; Score 61.5; DB 2; Length 1005;
Best Local Similarity 78.6%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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Db 551 KET-WETWTEYWQ 563
RESULT 7
US-08-463-210-9
; Sequence 9, Application US/08463210
; Patent No. 6001977
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
; APPLICANT: GALLO, Robert C.
; APPLICANT: WONG-STAAI, Flossie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,210
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/693,866
; FILING DATE: 23-JAN-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/659,339
; FILING DATE: 10-OCT-1984
; ATTORNEY/AGENT INFORMATION:
; NAME: Serunian, Leslie A.
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4193US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1015 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: HTLV-III
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1015
; OTHER INFORMATION: /note= "pol protein of HTLV-III"
US-08-463-210-9
Query Match 45.6%; Score 61.5; DB 3; Length 1015;
Best Local Similarity 78.6%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
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Db 562 KET-WETWTEYWQ 574
RESULT 8
US-09-124-900-3
; Sequence 3, Application US/09124900

Patent No. 6268484
GENERAL INFORMATION:
APPLICANT: KATINGER, Hermann
APPLICANT: BUCHACHER, Andrea
APPLICANT: ERNST, Wolfgang
APPLICANT: BALLAUN, Claudia
APPLICANT: PURTSCHER, Martin
APPLICANT: TEKOLA, Alexandra
APPLICANT: PREDL, Renate
APPLICANT: SCHMATZ, Christine
APPLICANT: KLIMA, Annelies
APPLICANT: STEINDL, Franz
APPLICANT: MUSTER, Thomas
TITLE OF INVENTION: HIV-Vaccines
FILE REFERENCE: 1939-112P
CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: PCT/EP95/01481
PRIOR FILING DATE: 1995-04-19
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 1015
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
-09-124-900-3

Query Match 45.6%; Score 61.5; DB 3; Length 1015;
Best Local Similarity 78.6%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
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562 KET-WETWTEYWQ 574

SULT 9
-08-463-028-9
Sequence 9, Application US/08463028
Patent No. 6610476
GENERAL INFORMATION:
APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STAAI, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US3
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HTLV-III
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1015
OTHER INFORMATION: /note= "pol protein of HTLV-III"
US-08-463-028-9

Query Match 45.6%; Score 61.5; DB 4; Length 1015;
Best Local Similarity 78.6%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
||| |||||:
Db 562 KET-WETWTEYWQ 574

RESULT 10
US-07-743-357-2
Sequence 2, Application US/07743357
Patent No. 5858646
GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-0045
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE: Human immunodeficiency virus type 1

STRAIN: BH102
07-743-357-2

Query Match 45.6%; Score 61.5; DB 2; Length 1016;
Best Local Similarity 78.6%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWTEWSQ 14
||| |||||:|
562 KET-WETWTEYWQ 574

ULT 11
07-743-357-3
Sequence 3, Application US/07743357
Patent No. 5858646

GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990

ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-0045

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
STRAIN: PV22

US-07-743-357-4

Query Match 45.6%; Score 61.5; DB 2; Length 1016;
Best Local Similarity 78.6%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
||| |||||:|
Db 562 KET-WETWTEYWQ 574

RESULT 13
US-07-743-357-5
Sequence 5, Application US/07743357
Patent No. 5858646

GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

Patent No. 5858646

GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990

ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-0045

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
STRAIN: PV22

US-07-743-357-4

Query Match 45.6%; Score 61.5; DB 2; Length 1016;
Best Local Similarity 78.6%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 KETWETWTEWSQ 14
||| |||||:|
Db 562 KET-WETWTEYWQ 574

RESULT 13
US-07-743-357-5
Sequence 5, Application US/07743357
Patent No. 5858646

GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-0045
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
STRAIN: BRU
US-07-743-357-5

Query Match 45.6%; Score 61.5; DB 2; Length 1016;
Best Local Similarity 78.6%; Pred. No. 3.1;
Matches 11; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

1 KETWETWWTWSQ 14
|||||
562 KET-WETWWTWYQ 574

SULT 14
-07-743-357-6
Sequence 6, Application US/077433357
Patent No. 5858646
GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-0045
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
STRAIN: MN
US-07-743-357-6

Query Match 44.8%; Score 60.5; DB 2; Length 913;
Best Local Similarity 76.9%; Pred. No. 3.7;
Matches 10; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 KETWETWWTWS 13
|||||
Db 459 KET-WETWWTWY 470

RESULT 15
US-07-743-357-8
Sequence 8, Application US/077433357
Patent No. 5858646
GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-0045
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus type 1
STRAIN: RF
US-07-743-357-8

Query Match 41.9%; Score 56.5; DB 2; Length 1003;
Est Local Similarity 71.4%; Pred. No. 13;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
1 KETWWETWWTEWSQ 14
|||||:|
549 KET-WEAWWTEYWQ 561

rch completed: February 25, 2004, 14:49:22
time : 25 secs

-09-915-914B-36
Sequence 36, Application US/09915914B
Publication No. US20030119725A1
GENERAL INFORMATION:
APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
APPLICANT: Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Horndorp, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
-09-915-914B-36
Query Match 100.0%; Score 135; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KETWETWWTWTSQPKKKRKV 21
|||||
1 KETWETWWTWTSQPKKKRKV 21
|||
RESULT 3
-10-226-956-291
Sequence 291, Application US/10226956
Publication No. US20030060399A1
GENERAL INFORMATION:
APPLICANT: Brophy, Colleen
APPLICANT: Komalavillas, Padmini
APPLICANT: Panitch, Alyssa
APPLICANT: Joshi, Lokesh
APPLICANT: Seal, Brandon L.
TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
FILE REFERENCE: ASU-1061-US
CURRENT APPLICATION NUMBER: US/10/226,956
CURRENT FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 60/314,535
PRIOR FILING DATE: 2001-08-23
NUMBER OF SEQ ID NOS: 320
SOFTWARE: PatentIn version 3.1
SEQ ID NO 291
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
-10-226-956-291
Query Match 100.0%; Score 135; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KETWETWWTWTSQPKKKRKV 21
|||||
1 KETWETWWTWTSQPKKKRKV 21
|||
RESULT 4
-10-077-555-13

-09-915-914B-36
Sequence 36, Application US/09915914B
Publication No. US20030077289A1
GENERAL INFORMATION:
APPLICANT: Wang, Rong-fu
TITLE OF INVENTION: Use of Cell-Penetrating Peptides to Generate Antitumor Immunity
FILE REFERENCE: P02373US1/10200806
CURRENT APPLICATION NUMBER: US/10/077,555
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/268,687
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-10-077-555-13
Query Match 100.0%; Score 135; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KETWETWWTWTSQPKKKRKV 21
|||||
1 KETWETWWTWTSQPKKKRKV 21
|||
RESULT 5
US-10-211-088-309
Sequence 309, Application US/10211088
Publication No. US20030104479A1
GENERAL INFORMATION:
APPLICANT: Bright, Gary R.
APPLICANT: Premkumar, D. David
APPLICANT: Chen, Yih-Tai
TITLE OF INVENTION: NO. US20030104479A1el Fusion Proteins And Assays For Molecular Bir
FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/341,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 309
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Protein-derived transport peptide
US-10-211-088-309
Query Match 100.0%; Score 135; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KETWETWWTWTSQPKKKRKV 21
|||||
1 KETWETWWTWTSQPKKKRKV 21
|||
RESULT 6
US-10-405-339-32
Sequence 32, Application US/10405339
Publication No. US20030190364A1
GENERAL INFORMATION:
APPLICANT: Panitch, Alyssa
APPLICANT: Seal, Brandon
TITLE OF INVENTION: Biological Affinity Based Delivery Systems
FILE REFERENCE: 9138-0079US

CURRENT APPLICATION NUMBER: US/10/405,339
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/369,568
PRIOR FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
EQ ID NO 32
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
10-405-339-32

Query Match 100.0%; Score 135; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KETWETWTEWSQPKKRV 21
|||||
1 KETWETWTEWSQPKKRV 21

SULT 7
10-360-275-37
Sequence 37, Application US/10360275
Publication No. US2004001464A1
GENERAL INFORMATION:
APPLICANT: Active Motif
APPLICANT: Efimov, Vladimir
APPLICANT: Fernandez, Joseph
APPLICANT: Archdeacon, Dorothy
APPLICANT: Archdeacon, John
APPLICANT: Choob, Mikhail

TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: AM102.P.1.1.1US
CURRENT APPLICATION NUMBER: US/10/360,275
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 10/072,975
PRIOR FILING DATE: 2002-02-09
PRIOR APPLICATION NUMBER: US 09/805,296
PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: US 60/189,190
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
10-360-275-37

Query Match 100.0%; Score 135; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KETWETWTEWSQPKKRV 21
|||||
1 KETWETWTEWSQPKKRV 21

SULT 8
10-372-003A-30
Sequence 30, Application US/10372003A
Publication No. US20030215846A1
GENERAL INFORMATION:
APPLICANT: Watt, Paul
APPLICANT: Thomas, Wayne
APPLICANT: Hopkins, Richard
TITLE OF INVENTION: Methods of constructing and screening

TITLE OF INVENTION: diverse expression libraries
FILE REFERENCE: FBRI40.001CP1
CURRENT APPLICATION NUMBER: US/10/372,003A
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/568,229
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,711
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic Pept peptide
US-10-372-003A-30

Query Match 94.1%; Score 127; DB 15; Length 21;
Best Local Similarity 95.2%; Pred. No. 3.7e-08;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KETWETWTEWSQPKKRV 21
|||||
Db 1 KETWETWTEWSQKKKRV 21

RESULT 9
US-09-915-914B-16
Sequence 16, Application US/09915914B
Publication No. US20030119725A1
GENERAL INFORMATION:
APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
APPLICANT: Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Hornorp, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
NAME/KEY: MISC FEATURE
LOCATION: (10)..(10)
OTHER INFORMATION: X can be any amino acid or no amino acid
NAME/KEY: MISC FEATURE
LOCATION: (11)..(11)
OTHER INFORMATION: X can be any amino acid or no amino acid
US-09-915-914B-16

Query Match 91.9%; Score 124; DB 10; Length 21;
Best Local Similarity 90.5%; Pred. No. 8.2e-08;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KETWETWTEWSQPKKRV 21
|||||
Db 1 KETWETWXXWSQPKKRV 21

RESULT 10
US-09-915-914B-10
Sequence 10, Application US/09915914B

Publication No. US20030119725A1
GENERAL INFORMATION:
APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
APPLICANT: Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Horndorp, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
-09-915-914B-10

Query Match 91.1%; Score 123; DB 10; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
1 KETWETWETWTSQPKKKRKV 21
||||||| |||||||||
1 KETWETWETWTSQPKKKRKV 21

SULT 11
-09-915-914B-8
Sequence 8, Application US/09915914B
Publication No. US20030119725A1
GENERAL INFORMATION:
APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
APPLICANT: Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Horndorp, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
-09-915-914B-8

Query Match 88.9%; Score 120; DB 10; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
1 KETWETWETWTSQPKKKR 19
||||||| |||||||||
1 KETWETWETWTSQPKKKR 19

RESULT 12
S-09-915-914B-12

Sequence 12, Application US/09915914B
Publication No. US20030119725A1
GENERAL INFORMATION:
APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
APPLICANT: Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Horndorp, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
US-09-915-914B-12

Query Match 80.0%; Score 108; DB 10; Length 19;
Best Local Similarity 88.9%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 WWETWETWTSQPKKKRKV 21
||||||| |||||||||
Db 2 WWETWETWTSQPKKKRKV 19

RESULT 13
US-09-915-914B-9
Sequence 9, Application US/09915914B
Publication No. US20030119725A1
GENERAL INFORMATION:
APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
APPLICANT: Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Horndorp, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
US-09-915-914B-9

Query Match 78.5%; Score 106; DB 10; Length 20;
Best Local Similarity 84.2%; Pred. No. 8.8e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KETWETWETWTSQPKKKR 19
||||||| |||||||||
Db 1 KETWETWETWTSQPKKKR 19

RESULT 14

Search completed: February 25, 2004, 14:53:45
Job time : 36 secs

09-915-914B-37
Sequence 37, Application US/09915914B
Publication No. US20030119725A1
GENERAL INFORMATION:
APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
APPLICANT: Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Horndorp, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
09-915-914B-37
Query Match 78.1%; Score 105.5; DB 10; Length 20;
Best Local Similarity 85.7%; Pred. No. 1e-05;
Matches 18; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
1 KETWETWETWSQPKKKRKV 21
1 KETWETWETWSQ-KKKRKV 20

BULT 15
09-915-914B-11
Sequence 11, Application US/09915914B
Publication No. US20030119725A1
GENERAL INFORMATION:
APPLICANT: Divita, Gilles
APPLICANT: Fernandez, Joseph
APPLICANT: Heitz, Frederic
APPLICANT: Morris, May
APPLICANT: Mery, Jean
APPLICANT: Archdeacon, John
APPLICANT: Horndorp, Kyle
TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS
FILE REFERENCE: AM-00105.P.1.1
CURRENT APPLICATION NUMBER: US/09/915,914B
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,932
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
09-915-914B-11

Query Match 75.6%; Score 102; DB 10; Length 19;
Best Local Similarity 85.7%; Pred. No. 2.4e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
1 KETWETWETWSQPKKKRKV 21
1 KETWETW--TWSQPKKKRKV 19